

QY 301 DKY:ETPDGDRNEHAHFQKAKERLEAKHRERMSQVMPREWEAFQAKNLPKAKKAVIQHF 360
DB 301 DKY:ETPDGDRNEHAHFQKAKERLEAKHRERMSQVMPREWEAFQAKNLPKAKKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITIALQAVPPRRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITIALQAVPPRRPHVFNMLK 420
QY 421 KYVRAEQDKRQHTLKHFHEVHMVDPKKAQIRSQVMTLHVYERMNQSLSLYVNPVAVA 480
DB 421 KYVRAEQDKRQHTLKHFHEVHMVDPKKAQIRSQVMTLHVYERMNQSLSLYVNPVAVA 480
QY 481 BEIQDEVDELQKQKQNTSDVLANMI:SEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
DB 481 BEIQDEVDELQKQKQNTSDVLANMI:SEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
QY 541 DDLQPMHSGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNKTETSEVKKMDAEF 600
DB 541 DDLQPMHSGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNKTETSEVKKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGV:ATVIVITLVMKKKQYTS:HHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGV:ATVIVITLVMKKKQYTS:HHGV 660
QY 661 VEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMONKK 697

RESULT 2

US-09-548-367D-16
; Sequence 16, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 6C/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVONGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOJITNNVEANQPVTIONCKRGRKQCKTHPHFVYPCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELOJITNNVEANQPVTIONCKRGRKQCKTHPHFVYPCVLG 120
QY 121 EFVSDALLVPCKKELHQRMDVOCETHLHWHTYAKETCSKSNLHDIYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPCKKELHQRMDVOCETHLHWHTYAKETCSKSNLHDIYGMLLPCGIDKFR 180

QY 181 GVFEVCCFJAEESDNVDSADAEEDSDVVMWGGADTDYADGSEDKVYVEVAEEVAEVEE 240
DB 181 GVFEVCCFJAEESDNVDSADAEEDSDVVMWGGADTDYADGSEDKVYVEVAEEVAEVEE 240
QY 241 EANDDEDDGDEVEEAEPEYEATERITSTATTTTTTIESVEEVVVRVPTTAASTPDVAV 300
DB 241 EANDDEDDGDEVEEAEPEYEATERITSTATTTTTTIESVEEVVVRVPTTAASTPDVAV 300
QY 301 DKYLETPGDNEHAHFQKAKERLEAKHRERMSQVMPREWEAFQAKNLPKAKKAVIQHF 360
DB 301 DKYLETPGDNEHAHFQKAKERLEAKHRERMSQVMPREWEAFQAKNLPKAKKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITIALQAVPPRRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITIALQAVPPRRPHVFNMLK 420
QY 421 KYVRAEQDKRQHTLKHFHEVHMVDPKKAQIRSQVMTLHVYERMNQSLSLYVNPVAVA 480
DB 421 KYVRAEQDKRQHTLKHFHEVHMVDPKKAQIRSQVMTLHVYERMNQSLSLYVNPVAVA 480
QY 481 BEIQDEVDELQKQKQNTSDVLANMI:SEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
DB 481 BEIQDEVDELQKQKQNTSDVLANMI:SEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
QY 541 DDLQPMHSGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNKTETSEVKKMDAEF 600
DB 541 DDLQPMHSGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNKTETSEVKKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGV:ATVIVITLVMKKKQYTS:HHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGV:ATVIVITLVMKKKQYTS:HHGV 660
QY 661 VEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMONKK 697

RESULT 3

US-09-551-953D-16
; Sequence 16, Application US/09551953D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-953D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVONGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOJITNNVEANQPVTIONCKRGRKQCKTHPHFVYPCVLG 120

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Db 61 TCIDTKEGILQCYQEVYPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTGYADGSEKXVEVAEVEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTGYADGSEKXVEVAEVEEVAEVEE 240
QY 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
Db 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
QY 301 DKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
Db 301 DKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEGEAANEKQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420
Db 361 QEKVESLEGEAANEKQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNOSLSLYNVPVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNOSLSLYNVPVA 480
QY 481 BEIQDEVDLLOKEQNSDDVLANMISEPRIISYNDALMPSLTETKTIVELLPVNGEFSL 540
Db 481 BEIQDEVDLLOKEQNSDDVLANMISEPRIISYNDALMPSLTETKTIVELLPVNGEFSL 540
QY 541 DDLQPMHSEFGADSVDPANTENEVEVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
Db 541 DDLQPMHSEFGADSVDPANTENEVEVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
QY 601 RHDSCYEVHHQKLVFFAEVGSNGKAIIGLMVGGVATVITVITLMLKKKQYTSIHGV 660
Db 601 RHDSCYEVHHQKLVFFAEVGSNGKAIIGLMVGGVATVITVITLMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697
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RESULT 4

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US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/JS99/2088:
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-20
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Query Match

Best Local Similarity 99.9%; Score 3646; DB 4; Length 697;

US-09-548-372D-20 Pred. No. 3.7e-264;

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Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAPQIAMFCGRLLNMHNMNVONGKWDSPSGTK 60
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAPQIAMFCGRLLNMHNMNVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQCYQEVYPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCVLG 120
Db 61 TCIDTKEGILQCYQEVYPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTGYADGSEKXVEVAEVEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTGYADGSEKXVEVAEVEEVAEVEE 240
QY 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
Db 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
QY 301 DKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
Db 301 DKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEGEAANEKQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420
Db 361 QEKVESLEGEAANEKQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNOSLSLYNVPVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNOSLSLYNVPVA 480
QY 481 BEIQDEVDLLOKEQNSDDVLANMISEPRIISYNDALMPSLTETKTIVELLPVNGEFSL 540
Db 481 BEIQDEVDLLOKEQNSDDVLANMISEPRIISYNDALMPSLTETKTIVELLPVNGEFSL 540
QY 541 DDLQPMHSEFGADSVDPANTENEVEVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
Db 541 DDLQPMHSEFGADSVDPANTENEVEVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
QY 601 RHDSCYEVHHQKLVFFAEVGSNGKAIIGLMVGGVATVITVITLMLKKKQYTSIHGV 660
Db 601 RHDSCYEVHHQKLVFFAEVGSNGKAIIGLMVGGVATVITVITLMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697
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RESULT 5

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US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
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; LENGTH: 697
; TYPE: Prt
; ORGANISM: Homo sapiens
; CS-09-548-367D-20

Query Match      99.9%  Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%  Pred. No. 3,70-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNMMNVQNGKWDSDSGTK 60
DB 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNMMNVQNGKWDSDSGTK 60
QY 61 TCIDTREGILQYCOEYYPE-QITNVVEANOPVTIQNCKRGRKQCKTHPHFVPIYRCLVG 120
DB 61 TCIDTREGILQYCOEYYPE-QITNVVEANOPVTIQNCKRGRKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSEKSTNLHDYGMCLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSEKSTNLHDYGMCLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEEVEE 240
QY 241 EADDEDDGDEVEEAEPEEATERTISATTTTTSVEEVVVRVPTTAASPDVAV 300
DB 241 EADDEDDGDEVEEAEPEEATERTISATTTTTSVEEVVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRERMSQVMREWEAEAEQAKNLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHRERMSQVMREWEAEAEQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVIVERNQSLSLYNNPVA 480
DB 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVIVERNQSLSLYNNPVA 480
QY 481 EEIQDEVELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFSL 540
DB 481 EEIQDEVELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFSL 540
QY 541 DDLCQPHSFAGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETELSEVKMDAEF 600
DB 541 DDLCQPHSFAGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETELSEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQVTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQVTSIHGV 660
QY 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697

RESULT 6
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 299/562801
; CURRENT APPLICATION NUMBER: US/09/551,853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,453
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 03/404,133
; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: Prt
; ORGANISM: Homo sapiens
; US-09-551-853D-20

Query Match      99.9%  Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%  Pred. No. 3,70-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNMMNVQNGKWDSDSGTK 60
DB 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNMMNVQNGKWDSDSGTK 60
QY 61 TCIDTREGILQYCOEYYPE-QITNVVEANOPVTIQNCKRGRKQCKTHPHFVPIYRCLVG 120
DB 61 TCIDTREGILQYCOEYYPE-QITNVVEANOPVTIQNCKRGRKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSEKSTNLHDYGMCLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSEKSTNLHDYGMCLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEEVEE 240
QY 241 EADDEDDGDEVEEAEPEEATERTISATTTTTSVEEVVVRVPTTAASPDVAV 300
DB 241 EADDEDDGDEVEEAEPEEATERTISATTTTTSVEEVVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRERMSQVMREWEAEAEQAKNLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHRERMSQVMREWEAEAEQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVIVERNQSLSLYNNPVA 480
DB 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVIVERNQSLSLYNNPVA 480
QY 481 EEIQDEVELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFSL 540
DB 481 EEIQDEVELLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFSL 540
QY 541 DDLCQPHSFAGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETELSEVKMDAEF 600
DB 541 DDLCQPHSFAGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETELSEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQVTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQVTSIHGV 660
QY 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697

RESULT 7
US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF

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; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-18

Query Match      99.8%   Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%   Pred. No. 6.2e-264;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNVQNGKWDSPSGTK 60
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DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKCKCTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPCKCFLEHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPCKCFLEHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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DB 181 GVEFVCCPLAESDNVDSADAEDDDSDVMWGGADTDYADGSEDKVVEAEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTITTESVEEVVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTITTESVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVWREWEAEERQAKNLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVWREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVENMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVDPKKAQIRSOVMTHLRVLYERMNQSLSLLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRVDPKKAQIRSOVMTHLRVLYERMNQSLSLLYNYPAVA 480
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DB 481 FEIQDEVDLLOKQNYSCDVLNMISEPRISYGNDAIMPSTETKTITVELLPVNGEFSL 540
QY 541 DDLQPHWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
DB 541 DDLQPHWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMWGVVVIATVITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMWGVVVIATVITLVMKKKQYTSIHGV 660
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QY 661 VEVDAAVTPERRHLSKMOGNGYENPTYKFEQMONKK 697
|||||
Db 661 VEVDAAVTPERRHLSKMOGNGYENPTYKFEQMONKK 697

RESULT 9
US-09-551-853D-18
: Sequence 18, Application US/09551853D
: Patent No. 6500667
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: FILE REFERENCE: 29915/6280L
: CURRENT APPLICATION NUMBER: US/09/551.853D
: CURRENT FILING DATE: 2000-04-18
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-551-853D-18

Query Match 99.8%; Score 3643; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 6.2e-264;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPTQAMFCGRNLNMHMVQNGKWDSPSGTK 60
|||||
Db 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPTQAMFCGRNLNMHMVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCEVPELOITNVVEANQVPTQNMCKRGRKCKTHPHFVPIYRCLVG 120
|||||
Db 61 TCIDTKEGILQYCEVPELOITNVVEANQVPTQNMCKRGRKCKTHPHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCFLHOERDMVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|||||
Db 121 EFVSDALLVPDKCFLHOERDMVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 161 GVEFYCCPLAESNDVDSADAEEDSDVMWGGADTDVADGSEKVVVEVAEEVAEEV 240
|||||
Db 161 GVEFYCCPLAESNDVDSADAEEDSDVMWGGADTDVADGSEKVVVEVAEEVAEEV 240

QY 241 EADDDEDEDEGEVEEAEAEYEAETRTSIA:TTTTTSEVGVVPTTAASTFDAY 300
|||||
Db 241 EADDDEDEDEGEVEEAEAEYEAETRTSIA:TTTTTSEVGVVPTTAASTFDAY 300

QY 301 DKYLETPGDENEHAFQKAKERLAKIRHRSQVWRWEEAEPCAKNLKALKKAV:QHP 360
|||||
Db 301 DKYLETPGDENEHAFQKAKERLAKIRHRSQVWRWEEAEPCAKNLKALKKAV:QHP 360

QY 361 QUKVESLQEAENRHOQVETHMARVEAMLDNRRLALENYITIALQAVPPRPHEVFNMLK 420
|||||
Db 361 QUKVESLQEAENRHOQVETHMARVEAMLDNRRLALENYITIALQAVPPRPHEVFNMLK 420

QY 421 KVVRAEQDRQHTLKHFEHVRWDPKAAQIRSOVMTHLVIVYERMNCSLSLYNYPAVA 480
|||||
Db 421 KVVRAEQDRQHTLKHFEHVRWDPKAAQIRSOVMTHLVIVYERMNCSLSLYNYPAVA 480

QY 481 EBIQDEVDELLOKEQNSDWLANNISEPRIISYNDALMPSLTETKTIVELPVNGEFSL 540
|||||
Db 481 EBIQDEVDELLOKEQNSDWLANNISEPRIISYNDALMPSLTETKTIVELPVNGEFSL 540
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QY 541 DDLOPWHSGADSVPAANTENEVEVDARPAADRLTTRPGSLTNKTEEISEVKMDAEF 600
|||||
Db 541 DDLOPWHSGADSVPAANTENEVEVDARPAADRLTTRPGSLTNKTEEISEVKMDAEF 600

QY 601 RHDGSEYVHHQKLVFFAEVDGSGNKGAIIGLVGSGVVIATVITLVMLKKKQVTSIHGV 660
|||||
Db 601 RHDGSEYVHHQKLVFFAEVDGSGNKGAIIGLVGSGVVIATVITLVMLKKKQVTSIHGV 660

QY 661 VEVDAAVTPERRHLSKMOGNGYENPTYKFEQMONKK 697
|||||
Db 661 VEVDAAVTPERRHLSKMOGNGYENPTYKFEQMONKK 697

RESULT 10
US-08-123-702-2
: Sequence 2, Application US/08123702
: Patent No. 5604131
: GENERAL INFORMATION:
: APPLICANT: Wadsworth, Samuel
: APPLICANT: Snyder, Benjamin
: APPLICANT: Reddy, Vermuri, B.
: APPLICANT: Wei, Chamer
: TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding Ap7770
: Patent No. 5604131
: TITLE OF INVENTION: Containing a Genomic DNA Insert of the XI and OX-2 Regio
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patricia L. Pabst
: STREET: 280C One Atlantic Center
: CITY: Atlanta
: STATE: GA
: COUNTRY: USA
: ZIP: 30309-3450
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: 17-SEPT-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patricia L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: TS1121
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404)-873-8794
: TELEFAX: (404)-873-8795
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-123-702-2

Query Match 99.7%; Score 3641; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPTQAMFCGRNLNMHMVQNGKWDSPSGTK 60
|||||
Db 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPTQAMFCGRNLNMHMVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCEVPELOITNVVEANQVPTQNMCKRGRKCKTHPHFVPIYRCLVG 120
|||||
Db 61 TCIDTKEGILQYCEVPELOITNVVEANQVPTQNMCKRGRKCKTHPHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCFLHOERDMVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|||||
Db 121 EFVSDALLVPDKCFLHOERDMVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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QY 181 GVEFYCCPLAEEUNVDSADAEEDSDVWVGADTDVAGSDEKVKVEVAEEERVAEVEE 240
DB 181 GVEFYCCPLAEEUNVDSADAEEDSDVWVGADTDVAGSDEKVKVEVAEEERVAEVEE 240
QY 241 EADDEDEDEDEVEEAEPEYEATERTISATITTTTTSSVEEVRVPTTAASTPDV 300
DB 241 EADDEDEDEDEVEEAEPEYEATERTISATITTTTTSSVEEVRVPTTAASTPDV 300
QY 301 DKYLETGPDGNEHAHFQAKERLEAKHRMSQVMEEREAERQAKNLPKADKAVIQHF 360
DB 301 DKYLETGPDGNEHAHFQAKERLEAKHRMSQVMEEREAERQAKNLPKADKAVIQHF 360
QY 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNLK 420
DB 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLLYNVPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLLYNVPVA 480
QY 481 EEIQDEVDLLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGEESL 540
DB 481 EEIQDEVDLLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGEESL 540
QY 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSLTNKTEISEVKMDAEF 600
DB 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSLTNKTEISEVKMDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVLMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVLMLKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMN 695
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMN 695
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RESULT 11

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US-08-104-165-1
: Sequence 1, Application US/08104165
: Patent No. 5877015
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: GOATE, Allison Mary
: APPLICANT: MOLLAN, Michael John
: APPLICANT: CHARTIER-HARLIN, Marie-Christine
: APPLICANT: OWEN, Michael John
: TITLE OF INVENTION: Test and Model for Alzheimer's Disease
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Khourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/104,165
: FILING DATE: 21-JAN-1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 9101:07.8
: FILING DATE: 21-JAN-1991
: APPLICATION NUMBER: 911845.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
```

```
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-104-165-1
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Query Match 99.7%; Score 3641; DB 2: Length 695;

Best Local Similarity 100.0%; Pred. No. 8.7e-264;

Mismatches 695; Conservative 0; Indels 0; Gaps 0;

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QY 1 MLPGIALALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVQNGKWDSPGSK 60
DB 1 MLPGIALALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVQNGKWDSPGSK 60
QY 61 TCIDTKESILQYCOEYVPELQITNVVEANQVPTIIONMCKRCKOCKT8PHFVPIRCLVG 120
DB 61 TCIDTKESILQYCOEYVPELQITNVVEANQVPTIIONMCKRCKOCKT8PHFVPIRCLVG 120
QY 121 EFVSDAILVDPKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDAILVDPKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFYCCPLAEEUNVDSADAEEDSDVWVGADTDVAGSDEKVKVEVAEEERVAEVEE 240
DB 181 GVEFYCCPLAEEUNVDSADAEEDSDVWVGADTDVAGSDEKVKVEVAEEERVAEVEE 240
QY 241 EADDEDEDEDEVEEAEPEYEATERTISATITTTTTSSVEEVRVPTTAASTPDV 300
DB 241 EADDEDEDEDEVEEAEPEYEATERTISATITTTTTSSVEEVRVPTTAASTPDV 300
QY 301 DKYLETGPDGNEHAHFQAKERLEAKHRMSQVMEEREAERQAKNLPKADKAVIQHF 360
DB 301 DKYLETGPDGNEHAHFQAKERLEAKHRMSQVMEEREAERQAKNLPKADKAVIQHF 360
QY 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNLK 420
DB 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLLYNVPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLLYNVPVA 480
QY 481 EEIQDEVDLLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGEESL 540
DB 481 EEIQDEVDLLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGEESL 540
QY 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSLTNKTEISEVKMDAEF 600
DB 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSLTNKTEISEVKMDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVLMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVLMLKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMN 695
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMN 695
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RESULT 12

```
US-08-464-250-1
: Sequence 1, Application US/08464250
: Patent No. 6107542
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: GOATE, Allison Mary
```

APPLICANT: MULLAN, Michael John
 APPLICANT: CHARTIER-HARLIN, Marie-Christine
 APPLICANT: OWEN, Michael John
 TITLE OF INVENTION: Test and Model for Alzheimer's Disease
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,250
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/104,165
 FILING DATE: 21-JAN-1992
 APPLICATION NUMBER: 9101307.8
 FILING DATE: 21-JAN-1991
 APPLICATION NUMBER: 9118445.7
 FILING DATE: 28-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebeschuetz, Joe
 REGISTRATION NUMBER: 37,505
 REFERENCE/DOCKET NUMBER: 16163-000100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 695 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 CS-08-464-250-1

Query Match 99.7% Score 3641; DH 3; Length 695;
 Best Local Similarity 100.0%; Pred. No. 8.7e-264;
 Matches 595; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQTAMFCGRINMIMYONGKNSDPSGTK 60
 DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQTAMFCGRINMIMYONGKNSDPSGTK 60
 QY 61 TCIDTKEGILQYCOEVPPELOITNVVEANOPVTQNNCKRGKCKCKTHPHFVTPYRCLVG 120
 DB 61 TCIDTKEGILQYCOEVPPELOITNVVEANOPVTQNNCKRGKCKCKTHPHFVTPYRCLVG 120
 QY 121 EFVSDALLVPCKKFLHOERMDVCEILHWHITVAKECCESEKSTNLHDYGMILPCTGCTKFR 180
 DB 121 EFVSDALLVPCKKFLHOERMDVCEILHWHITVAKECCESEKSTNLHDYGMILPCTGCTKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWKGADIDVADGSDKVVVAEEEEVAEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWKGADIDVADGSDKVVVAEEEEVAEVEE 240
 QY 241 EADDEDDEDEGEVEEAEFEYERATRTTSTTTTSTVESVEVVRVPTTAASTPDVAV 300
 DB 241 EADDEDDEDEGEVEEAEFEYERATRTTSTTTTSTVESVEVVRVPTTAASTPDVAV 300
 QY 301 DKYLETPGDENEHAHFQAKERLEAKKRRMSQVWREWEAEERAKNLPKADKAVTCHP 360
 DB 301 DKYLETPGDENEHAHFQAKERLEAKKRRMSQVWREWEAEERAKNLPKADKAVTCHP 360
 QY 361 QEKVESLFOEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKX 420

DB 361 QEKVESLFOEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKX 420
 QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTLRLVIYERMNQSLSLLYNVPAVA 480
 DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTLRLVIYERMNQSLSLLYNVPAVA 480
 QY 481 EBIQDEVELLQKEONYSDDVLANMISEPRISYGNDAIMPSTLTKTTVFLLPVNGEESL 540
 DB 481 EBIQDEVELLQKEONYSDDVLANMISEPRISYGNDAIMPSTLTKTTVFLLPVNGEESL 540
 QY 541 DDLQPMHSGALSVFANTHNEVEPYDARFADRGILITRPGSLTNKITEEISEVKMDAEF 600
 DB 541 DDLQPMHSGALSVFANTHNEVEPYDARFADRGILITRPGSLTNKITEEISEVKMDAEF 600
 QY 601 RHDSQYEVHHQKLVFAEDVSGNSKGAIGLIVGGVVIATVITLVMKKKQYTSIHHGV 660
 DB 601 RHDSQYEVHHQKLVFAEDVSGNSKGAIGLIVGGVVIATVITLVMKKKQYTSIHHGV 660
 QY 661 VEYDAAVTPERHLSKMOONGYENETKYKFFEQMN 695
 DB 661 VEYDAAVTPERHLSKMOONGYENETKYKFFEQMN 695
 RESULT 13
 US-08-464-250-1
 Sequence 1, Application US/08464250
 Patent No. 6300540
 GENERAL INFORMATION:
 APPLICANT: HARDY, John Anthony
 COATE, Alison Mary
 MULLAN, Michael John
 CHARTIER-HARLIN, Marie-Christine
 OWEN, Michael John
 TITLE OF INVENTION: Test and Model for Alzheimer's Disease
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,250
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/104,165
 FILING DATE: 21-JAN-1992
 APPLICATION NUMBER: 9101307.8
 FILING DATE: 21-JAN-1991
 APPLICATION NUMBER: 9118445.7
 FILING DATE: 28-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebeschuetz, Joe
 REGISTRATION NUMBER: 37,505
 REFERENCE/DOCKET NUMBER: 16163-000100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 695 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-08-464-250-1

Query Match 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNNVEANQPVTONMCKRGRKCKTHPHFVTPYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNNVEANQPVTONMCKRGRKCKTHPHFVTPYRCLVG 120
QY 121 EFVSUALLVPCKFLHGERMDVCETHLHWTVAKEICSEKSTNLHRYGMLLPCKGIDKFR 180
DB 121 EFVSUALLVPCKFLHGERMDVCETHLHWTVAKEICSEKSTNLHRYGMLLPCKGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEAEATERTTSIATTTTTTSTESVEEVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEAEATERTTSIATTTTTTSTESVEEVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
DB 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQDKRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLSLYNVPAVA 480
DB 421 KYVRAEQDKRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLSLYNVPAVA 480
QY 481 EIQDEVDLLOKEQNSDDVLANNISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
DB 481 EIQDEVDLLOKEQNSDDVLANNISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
QY 541 DDLQPHSFAGDSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTEESEVKMDAEF 600
DB 541 DDLQPHSFAGDSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTEESEVKMDAEF 600
QY 601 RHDGSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
DB 601 RHDGSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695

RESULT 14
US-09-458-481B-7
; Sequence 7, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
; APPLICANT: KUMAR, Vijaya B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
; FILE REFERENCE: 16153-9250
; CURRENT APPLICATION NUMBER: US/09/458,481B
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Monkey
US-09-458-481B-7

Query Match 99.7%; Score 3641; DB 4; Length 695;

Rest Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNNVEANQPVTONMCKRGRKCKTHPHFVTPYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNNVEANQPVTONMCKRGRKCKTHPHFVTPYRCLVG 120
QY 121 EFVSUALLVPCKFLHGERMDVCETHLHWTVAKEICSEKSTNLHRYGMLLPCKGIDKFR 180
DB 121 EFVSUALLVPCKFLHGERMDVCETHLHWTVAKEICSEKSTNLHRYGMLLPCKGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEAEATERTTSIATTTTTTSTESVEEVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEAEATERTTSIATTTTTTSTESVEEVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
DB 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQDKRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLSLYNVPAVA 480
DB 421 KYVRAEQDKRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLSLYNVPAVA 480
QY 481 EIQDEVDLLOKEQNSDDVLANNISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
DB 481 EIQDEVDLLOKEQNSDDVLANNISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
QY 541 DDLQPHSFAGDSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTEESEVKMDAEF 600
DB 541 DDLQPHSFAGDSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTEESEVKMDAEF 600
QY 601 RHDGSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
DB 601 RHDGSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695

RESULT 15
US-09-458-481B-8
; Sequence 8, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
; APPLICANT: KUMAR, Vijaya B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
; FILE REFERENCE: 16153-9250
; CURRENT APPLICATION NUMBER: US/09/458,481B
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-458-481B-8

Query Match 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTGAGNAGLLAPQIAMECGRINLKHMHNVONGKWDSDSGTK 60
DB 1 MLPGLALLLLAAWTAARALEVPTGAGNAGLLAPQIAMECGRINLKHMHNVONGKWDSDSGTK 60
QY 61 TCIDTKEGILQYCOEVYPELOITNVVEANOPVTIONCKKGRKOCKTHPHFVTPYRCIUG 120
DB 61 TCIDTKEGILQYCOEVYPELOITNVVEANOPVTIONCKKGRKOCKTHPHFVTPYRCIUG 120
QY 121 EFVSDALLVPCKCFIHOERMDVCETHLHMHVAKETCSKSTNLHDYGMILPFGIDKFR 180
DB 121 EFVSDALLVPCKCFIHOERMDVCETHLHMHVAKETCSKSTNLHDYGMILPFGIDKFR 180
QY 181 GVEFVCCPLAESDNVSADAEEDSDVWKGCCADTDYADGSEDKVVEVAKEEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVSADAEEDSDVWKGCCADTDYADGSEDKVVEVAKEEVEAEVEE 240
QY 241 EADDDDEDDEVEEAEPEYEATERTTSIATTTTTSVEEYVYVVTAASTPCAV 300
DB 241 EADDDDEDDEVEEAEPEYEATERTTSIATTTTTSVEEYVYVVTAASTPCAV 300
QY 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEWEAEEROAKNLPKADKKAV:OHF 360
DB 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEWEAEEROAKNLPKADKKAV:OHF 360
QY 361 QEKVESLEQEAANROQLVETHMARVEAMLNDRRLALENYITALOAVPPRPHVFNKJK 420
DB 361 QEKVESLEQEAANROQLVETHMARVEAMLNDRRLALENYITALOAVPPRPHVFNKJK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIERMNSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIERMNSLSLLYNVPAVA 480
QY 481 EEIODEVDEILQKQNSDDVLANNISEPRIISYNDALMPSLITETKTVEELLPVNGEFSI 540
DB 481 EEIODEVDEILQKQNSDDVLANNISEPRIISYNDALMPSLITETKTVEELLPVNGEFSI 540
QY 541 DDLOPWHSEFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
DB 541 DDLOPWHSEFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
QY 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLMVGGVIAIVIVITLVMKKKQYTSIHGGV 660
DB 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLMVGGVIAIVIVITLVMKKKQYTSIHGGV 660
QY 661 VEVDAAVTPEERHLSKMCNGENPTYKFFQOMQ 695
DB 661 VEVDAAVTPEERHLSKMCNGENPTYKFFQOMQ 695

the beta secretase site to produce amyloid beta peptide

Claim 132; page 137-141; 183pp; Ecq.ish.

This sequence represents a modified version of the human amyloid precursor protein (APP) amino acid sequence. The sequence is used in an example of the method of the invention, to show that modification of APP increases beta amyloid protein processing. The invention relates to a protease (e.g. Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DSG or LTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal trans-membrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in Alzheimer's disease.

Sequence 697 AA:

```
Query Match      100.0%; Score 3651; DB 21; Length: 697;
Best Local Similarity 100.0%; Pred. No. 1.7e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0;
```

QY	1	M L P G L A L L I L A A W T A R A L E V P T D C N A G L A E P Q I A M F C G R L N H M H M V O N G K W D S P S G T K	60
QY	1	M L P G L A L L I L A A W T A R A L E V P T D C N A G L A E P Q I A M F C G R L N H M H M V O N G K W D S P S G T K	60
QY	61	T C I D T K E G I L O Y C Q V Y P E L Q I I K V V F A N Q P V T I O N M C K R G K O C K T I H P H F V I P R C L V G	120
QY	61	T C I D T K E G I L O Y C Q V Y P E L Q I I K V V F A N Q P V T I O N M C K R G K O C K T I H P H F V I P R C L V G	120
QY	121	E V Y S D A L L V P O K C K F L H O E R M D V C E T H L H W H T V A K E T C S E K S N L H D Y G M L P C O I D K R F R	180
QY	121	E V Y S D A L L V P O K C K F L H O E R M D V C E T H L H W H T V A K E T C S E K S N L H D Y G M L P C O I D K R F R	180
QY	181	G Y E F V C C P L A E S D N V D S A D A E E D S D V M W G G A D T Y A D G S D K V E V A E E E F V A E V E S E	240
QY	181	G Y E F V C C P L A E S D N V D S A D A E E D S D V M W G G A D T Y A D G S D K V E V A E E E F V A E V E S E	240
QY	241	E A D D D E D D G D E V E E A E S Y E A T E R T I S A T I I T T T T S E V E V V R V P T T A A S T P D A V	300
QY	241	E A D D D E D D G D E V E E A E S Y E A T E R T I S A T I I T T T T S E V E V V R V P T T A A S T P D A V	300
QY	301	K Y L E T P G D E N H A H F Q A K E R L E A K I H R M S Q V M R E W E A F Q A K N I P K A K K A V I Q I H	360
QY	301	K Y L E T P G D E N H A H F Q A K E R L E A K I H R M S Q V M R E W E A F Q A K N I P K A K K A V I Q I H	360
QY	361	Q E K V E S L F O E A A N E R Q Q I V E T H M A R V E A M L N D R R L A L E N Y I T A C A V P P R P H V E N M L K	420
QY	361	Q E K V E S L F O E A A N E R Q Q I V E T H M A R V E A M L N D R R L A L E N Y I T A C A V P P R P H V E N M L K	420
QY	421	K Y V R A E Q D R Q H T L K H F E H V R M P O K K A Q I R S O V N T H L R V I T E R M N O S L I L E N Y P A V A	480
QY	421	K Y V R A E Q D R Q H T L K H F E H V R M P O K K A Q I R S O V N T H L R V I T E R M N O S L I L E N Y P A V A	480
QY	481	E E I Q D E V D E L L Q K E O N Y S D D V L A N K I S U P R I S Y G N D A L M P S L E T K T I T V E L L P V N G E S L	540
QY	481	E E I Q D E V D E L L Q K E O N Y S D D V L A N K I S U P R I S Y G N D A L M P S L E T K T I T V E L L P V N G E S L	540
QY	541	D O L O P H S F G A D S V P A N T E N E V P D A R P A D R G L T T P Q S G I T N I K T E I S E V K W A E F	600
QY	541	D O L O P H S F G A D S V P A N T E N E V P D A R P A D R G L T T P Q S G I T N I K T E I S E V K W A E F	600
QY	601	R H D S O Y E V H O K L V F F A E D V G S N K G A I I G M V G O W A T V I V I T L Y M L K K Q V T S I H W G	660
QY	601	R H D S O Y E V H O K L V F F A E D V G S N K G A I I G M V G O W A T V I V I T L Y M L K K Q V T S I H W G	660

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00 661 VEVDAAVTPEERHLSKMOONGYENPTYKFEFQMONKK 697
      | | | | | | | | | | | | | | | | | | | | | |
00 66: VEVDAAVTPEERHLSKMOONGYENPTYKFEFQMONKK 697

```

RESULT 2
AAE10635
ID AAE10635 standard; Protein: 697 AA.

AA
AC
AAE10635;

XX
DT 10-DEC-2001 (first entry)

XX
DE
Human amyloid protein precursor 695-KK (APP695-KK) isoform.

Human; aspartyl protease 1; Aspi; amyloid precursor protein; APP695-KK;
KW
Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW
amyloid plaque; neuronal loss; proteolytic; nontropic; neuroprotective;
KW
XX

XX OS Homo sapiens.

XX
SC
Synthetic.

GB233761-A.

PD C4-JUL-2001.
 XY

PF 22-SEP-2000; 2000GR-0023315.
YY

PR 23-SEP-1999: 99US-0155493.
 PP 23-SEP-1999: 99US-0404133.

PR 23-SEP-1999; 99WC-US20881.
03 13-OCT-1999; 99US-0415001

PR 06-DEC-1999; 99US-0169232.

PA (PHAA) PHARMACIA & UPJOHN C

P: Bienkowski MJ, Gurney M;

DR WP1; 2001-444208/48.

XX

amyloid precursor pr

pt disease -

Example 6: Page 114-116; 187pp; English.

CC The patent discloses human aspartyl prot

CC domain, or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC or the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC pro-cursor 695-KK (APP695-KK) isoform which is obtained by
CC the addition of two Lys residues (KK motif) at the C-terminus of
CC APP695 protein.

AA	Sequence	697 AA;
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Query Match	100.0%	Score 3651	DB 22	Length 697
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Best Local Similarity 100.0%; pred. No. 1./e-256;
Matches 697; Conservative C: Mismatches Q:

0v | MIPGIAI- IIAW...ABALEVPTDGNAGL IAFPCIAMFCGRINNHMNVONGKW)SDPSGTK 60


```
DB 1 MLPGALLLLAANTARALEVPTDGNAGLLASQIMFCGRNLNMHMYQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120
QY 121 EFVSDALLVPCKKFLHOERDMVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPCKKFLHOERDMVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDCGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVRVP:TAASIPDAV 300
DB 241 EADDEDEDCGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVRVP:TAASIPDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMEWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMEWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVNMLK 420
QY 421 KYVRAEQKDRHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMQS:SLLYNVFAVA 480
DB 421 KYVRAEQKDRHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMQS:SLLYNVFAVA 480
QY 481 BEIGDEVDLQKQNSYDVLANK:SEPR:SYGNDALMPSL:ETKTIYELLVNGEFSL 540
DB 481 BEIGDEVDLQKQNSYDVLANK:SEPR:SYGNDALMPSL:ETKTIYELLVNGEFSL 540
QY 541 DDLPQWHSFGADSPANTENEVEPVDARPAADRGITRPGSLN:IKTEE:SEVKM:AEF 600
DB 541 DDLPQWHSFGADSPANTENEVEPVDARPAADRGITRPGSLN:IKTEE:SEVKM:AEF 600
QY 601 RHDGSGYVHHOKLVFFAEIDVGSNGKAGLIGLVGGVVIATVIT:VMLKKQYIS:HHGV 660
DB 601 RHDGSGYVHHOKLVFFAEIDVGSNGKAGLIGLVGGVVIATVIT:VMLKKQYIS:HHGV 660
QY 661 VEVDAAVTPERHLSKMOQYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPERHLSKMOQYENPTYKFFEQMONKK 697
```

RESULT 3

AAE06855

XX AA E06865 standard; Protein: 697 AA.

XX AC AAE06865;

XX DT 23-Oct-2001 (first entry)

XX DE Human amyloid precursor protein 695-KK (APP695-KK) isoform.

XX KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;

KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; notropic;

KW neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;

XX KW

OS Homo sapiens.

XX PN WC200150829-A2.

XX XX

PD 19-JUL-2001.

XX XX

XX PF 09-MAY-2001; 2001WO-IB00799.

XX XX

XX PR 09-MAY-2001; 2001WO-IB00799.

```
XX PA (BIEN/) BIENKOWSKI M J.
PA (GJRN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX BIenkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R:
XX WPI: 2001-483072/52.
XX N-PSDB: AAD13027.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity.
XX
XX Example 6: Page 144-146; 185pp; English.
XX
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
XX precursor protein (APP) isoforms and their corresponding DNA molecules.
XX Human aspartyl proteases can act as beta-secretase proteases useful for
XX treating Alzheimer's disease. APP isoforms are useful for identifying
XX modulators of amyloid-beta peptide production, for use in designing
XX therapeutics for the treatment and prevention of Alzheimer's disease.
XX dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
XX and neuronal loss. APP isoforms are also used in methods for identifying
XX inhibitors and modulators of human Asp2 activity. The invention relates
XX to a method for identifying agents that modulate the activity of human
XX aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
XX as a means to screen in cellular assays for the inhibitors of beta- and
XX gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
XX polymerase chain reactions (PCR). The probes are useful for detecting
XX Hu-Asp nucleic acids in vitro assays and in Northern and Southern
XX blots. The present sequence is modified human amyloid precursor
XX protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
XX addition of two Lys residues (KK motif) at the C-terminal end of APP695
XX isoform.
XX
XX SQ Sequence 697 AA;
```

Query Match 100.0%; Score 3651; DB 22; Length 697;

Best local similarity 100.0%; Pred. No. 1.7e-256;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAANTARALEVPTDGNAGLLASQIMFCGRNLNMHMYQNGKWDSPSGTK 60

DB 1 MLPGALLLLAANTARALEVPTDGNAGLLASQIMFCGRNLNMHMYQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120

DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120

QY 121 EFVSDALLVPCKKFLHOERDMVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180

DB 121 EFVSDALLVPCKKFLHOERDMVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180

QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240

DB 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240

QY 241 EADDEDEDCGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVRVP:TAASIPDAV 300

DB 241 EADDEDEDCGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVRVP:TAASIPDAV 300

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMEWEAEERQAKNLPKADKAVIQHF 360

DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMEWEAEERQAKNLPKADKAVIQHF 360

QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVNMLK 420

DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVNMLK 420

QY 421 KYVRAEQKORHTLKHFEHVRMVDPKAAQIRSQWHLHLEVYERKNGSLSLYNVPAVA 480
 DB 421 KYVRAEQKORHTLKHFEHVRMVDPKAAQIRSQWHLHLEVYERKNGSLSLYNVPAVA 480
 QY 461 EETODEVELLQKEQNSDVLANNISEPRISYGNDAIMPSTLTKTIVVILLPVNGEFSL 540
 DB 461 EETODEVELLQKEQNSDVLANNISEPRISYGNDAIMPSTLTKTIVVILLPVNGEFSL 540
 QY 541 DOLQPHSEFCADSVDPANTENEVEPVDPARPAADRGLTTRPGSGITNLKTEEISEVKNDAEF 600
 DB 541 DOLQPHSEFCADSVDPANTENEVEPVDPARPAADRGLTTRPGSGITNLKTEEISEVKNDAEF 600
 QY 601 RHDSGVEVHHQKLVFFADYVGSNKGALGLMVGGVIAIVITIVMLKKKYTTHSGV 660
 DB 601 RHDSGVEVHHQKLVFFADYVGSNKGALGLMVGGVIAIVITIVMLKKKYTTHSGV 660
 QY 661 VEYDAAVTPPEERHLSKMGONGYENPTYKFFEQMONKK 697
 DB 661 VEYDAAVTPPEERHLSKMGONGYENPTYKFFEQMONKK 697

RESULT 4
 AAU06609
 ID AAU06609 standard; Protein: 697 AA.
 AC AAU06609;
 XT 24-OCT-2001 (first entry)
 XX Human Amyloid precursor protein mutant, APP695-KK.
 XX Human; Aspartyl protease; Asp2b; beta-secretase; nontropic;
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
 KW amyloid-beta; Abeta; APP695-KK; mutant; muten.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 696..697
 FT /note= "2 Extra Lys residues added compared to
 wild-type APP695"
 XX W0200149098-A2.
 XX 12-JUL-2001.
 XX 09-MAY-2001; 2001WO-1B00798.
 XX 09-MAY-2001; 2001WO-1B00798.
 XX (BIEN/) BIENKOWSKI M J.
 XX (GURN/) GURNEY M E.
 XX (HEIN/) HEINKINSON R L.
 XX (PARO/) PARODI L A.
 XX (YANR/) YAN R.
 XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R:
 WPI: 2001-502549/55.
 DR N-PSDB; AAS11523.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity
 XX Example 6: Page 144-146; 185pp; English.
 XX The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp

CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the App-Sw-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC Asp oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is the human
 CC APP695 mutant, APP695-KK which has 2 extra Lys residues added at
 CC the C-terminus compared to the wild-type APP695. The mutation alters the
 CC specificity of the APP gamma-secretase activity and increases the rate
 CC of processing of the amyloid Abeta peptide.

SO Sequence 697 AA;
 Query Match 100.0%; Score 3651; DB 22; Length 697;
 Best Local Similarity 100.0%; Pred. No. 1.7e-256;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHNVQNGKWDSDSGTK 60
 DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHNVQNGKWDSDSGTK 60
 QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGRKQCKTHPHFVYRCLVG 120
 DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGRKQCKTHPHFVYRCLVG 120
 QY 121 EFVSDALIVPCKCKFLHOERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALIVPCKCKFLHOERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAEESDNVDSADAEDDDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
 DB 181 GVEFVCCPLAEESDNVDSADAEDDDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
 QY 241 EADDDEDDGDEVEEAEPEEATEETTSIAITTTTTTESVEEVVVRPTTAASPTDVA 300
 DB 241 EADDDEDDGDEVEEAEPEEATEETTSIAITTTTTTESVEEVVVRPTTAASPTDVA 300
 QY 301 DKYLETPGDENEHAIFOKAKERLEAKHREMSVMREWEAEARQAKNLPKADKKAVIQHF 360
 DB 301 DKYLETPGDENEHAIFOKAKERLEAKHREMSVMREWEAEARQAKNLPKADKKAVIQHF 360
 QY 361 QEKVESLEGEAANEKQQLVETHMARVEAMLNDRKRLALENYITALQAVPPRPRHVMMLK 420
 DB 361 QEKVESLEGEAANEKQQLVETHMARVEAMLNDRKRLALENYITALQAVPPRPRHVMMLK 420
 QY 421 KYVRAEQKORHTLKHFEHVRMVDPKAAQIRSQWHLHLEVYERKNGSLSLYNVPAVA 480
 DB 421 KYVRAEQKORHTLKHFEHVRMVDPKAAQIRSQWHLHLEVYERKNGSLSLYNVPAVA 480
 QY 481 EETODEVELLQKEQNSDVLANNISEPRISYGNDAIMPSTLTKTIVVILLPVNGEFSL 540
 DB 481 EETODEVELLQKEQNSDVLANNISEPRISYGNDAIMPSTLTKTIVVILLPVNGEFSL 540
 QY 541 DOLQPHSEFCADSVDPANTENEVEPVDPARPAADRGLTTRPGSGITNLKTEEISEVKNDAEF 600
 DB 541 DOLQPHSEFCADSVDPANTENEVEPVDPARPAADRGLTTRPGSGITNLKTEEISEVKNDAEF 600
 QY 601 RHDSGVEVHHQKLVFFADYVGSNKGALGLMVGGVIAIVITIVMLKKKYTTHSGV 660
 DB 601 RHDSGVEVHHQKLVFFADYVGSNKGALGLMVGGVIAIVITIVMLKKKYTTHSGV 660


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XX PR 23-SEP-1999: 99US-0155493.
XX PR 23-SEP-1999: 99US-0155493.
XX PR 13-OCT-1999: 99US-0416901.
XX PR 06-DEC-1999: 99US-0169232.
XX PA (PRAA ) PHARMACIA & UPJOHN CO.
XX PI Gurney M, Bienkowski M;
XX XX WPI: 2001-290516/30.
XX DR N-PSDB; AAD06745.
XX PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX PT protein, useful for the treatment of Alzheimer's disease.
XX XX Example 5: Page 143-145; 189pp; English.
XX CC The present invention relates to enzymes for cleaving the alpha-
XX CC secretase site of the amyloid precursor protein (APP) and methods of
XX CC identifying those enzymes. The methods may be used to identify enzymes
XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
XX CC protein. The enzymes may be used to treat or modulate the progress of
XX CC Alzheimer's disease. The present sequence is human APP695-KK. This
XX CC sequence contains two carboxy-terminal lysine residues.
XX SQ Sequence 597 AA;
Query Match 100.0%; Score 3651; DB 22; Length 697;
Best Local Similarity 100.0%; Pred No.: 7e-256;
Matches 697; Conservative C; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPLGLALLAAWTAARALEVPTDNGAGLAEPOLAMFCGRIMNMNVQNGKWDSPSSTK 60
DB 1 MLPLGLALLAAWTAARALEVPTDNGAGLAEPOLAMFCGRIMNMNVQNGKWDSPSSTK 60
QY 61 TCIDTREGILOVCOEYVPELOITNVVEANOPTVIONMKGRKCKTTPHFVPEVCLVG 120
DB 61 TCIDTREGILOVCOEYVPELOITNVVEANOPTVIONMKGRKCKTTPHFVPEVCLVG 120
QY 121 EFVSDALLVPDKCKFLHQFQRMQVCEPHLHHTVAKPTCEKSLINLYCMLLPQSDCKR 180
DB 121 EFVSDALLVPDKCKFLHQFQRMQVCEPHLHHTVAKPTCEKSLINLYCMLLPQSDCKR 180
QY 181 GVEFVCCPLAEESNDVSDADAEDSDVWNGADTGYADSEKVFVEVAVAEVAFEE 240
DB 181 GVEFVCCPLAEESNDVSDADAEDSDVWNGADTGYADSEKVFVEVAVAEVAFEE 240
QY 241 EADDUDEDGDEVEFEAEPEPEFATERTTSATTITTESVEEVVRYPTTAATSTPAV 300
DB 241 EADDUDEDGDEVEFEAEPEPEFATERTTSATTITTESVEEVVRYPTTAATSTPAV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHREMSOVKRESEARQAKNLPKAKKAVIGHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHREMSOVKRESEARQAKNLPKAKKAVIGHF 360
QY 361 QEKVESIEQEAANERQOLVIEHMARVEAMLNDRRLALANYTALQVPPRPHVFNMLK 420
DB 361 QEKVESIEQEAANERQOLVIEHMARVEAMLNDRRLALANYTALQVPPRPHVFNMLK 420
QY 421 KYVRAEQKQKHTLKFEHVRMVDPKKAAGIRSOVWTHLVRYERNQSLLYNVAVA 480
DB 421 KYVRAEQKQKHTLKFEHVRMVDPKKAAGIRSOVWTHLVRYERNQSLLYNVAVA 480
QY 481 EEIQDEVDLLOXEOYSDVPLANNMSEPRISYVGNALMPSCTETKTVVLLPVNGEFS 540
DB 481 EEIQDEVDLLOXEOYSDVPLANNMSEPRISYVGNALMPSCTETKTVVLLPVNGEFS 540
QY 541 DOQPHSFSGADSVPAANTENEVEFVDPARPAADRLTTRPGSLINKITSEI SEVKNDAEF 600
DB 541 DOQPHSFSGADSVPAANTENEVEFVDPARPAADRLTTRPGSLINKITSEI SEVKNDAEF 600
QY 601 RHDSGYEVHQKLVFAEDVGSNKGAIIGLVGGVVIATVITLVMLKKOYTSIHGCV 660

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DB 501 RHDSGYEVHQKLVFAEDVGSNKGAIIGLVGGVVIATVITLVMLKKOYTSIHGCV 660
QY 661 VEYDAAVTPEERHESKMOONGYENPTYKFFEOMONKK 697
DB 661 VEYDAAVTPEERHESKMOONGYENPTYKFFEOMONKK 697
RESULT 7
ABB78596
ID ASB78596 standard; Protein; 697 AA.
XX AC ABB78596;
XX PT 16-Jul-2002 (first entry)
XX DE Human APP695-KK protein sequence SEQ ID NO:16.
XX KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
XX KW proteolytic; amyloid precursor protein; APP.
XX OS Homo sapiens.
XX EN S2367060-A.
XX XX 27-MAR-2002.
XX PF 29-OCT-2001; 2001GB-0025934.
XX PR 23-SEP-1999: 99US-155493P.
XX PR 23-SEP-1999: 99US-0404133.
XX PR 23-SEP-1999: 99US-020881.
XX PR 13-OCT-1999: 99US-0416901.
XX PR 06-DEC-1999: 99US-169232P.
XX PR 22-SEP-2000: 2000GB-0023315.
XX PA (PRAA ) PHARMACIA & UPJOHN CO.
XX PI Bienkowski M, Gurney M;
XX XX WPI: 2002-396337/43.
XX DR N-PSDB; ABL52463.
XX PT Human aspartyl protease 1 substrates useful in assays to detect
XX PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
XX PT Disease.
XX XX Example 6: Page 114-116; 182pp; English.
XX CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
XX CC substrate (1) which comprises a peptide of no more than 50 amino acids,
XX CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
XX CC Ala-Pro. Also described are: (i) a method (II) for assaying hu-Asp1
XX CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
XX CC (1) under acidic conditions; and (b) determining the level of hu-Asp1
XX CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
XX CC nucleotide sequence that hybridises under stringent conditions to the
XX CC non-coding strand complementary to a defined 1804 nucleotide sequence
XX CC (see ABL52463) where the nucleotide sequence encodes a polypeptide having
XX CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
XX CC domain; (3) a purified polynucleotide (III') comprising a sequence that
XX CC hybridises under stringent conditions to (III) (the nucleotide sequence
XX CC encodes a polypeptide further lacking a pro-peptide domain corresponding
XX CC to amino acids 23-62 of hu-Asp1 (see ABL78589)); (4) a vector (IV)
XX CC comprising (III) or (III') and (5) a host cell (V) transformed or
XX CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
XX CC substrate (1) may be used as an enzyme substrate in assays to detect
XX CC aspartyl protease activity, (II) and therefore diagnose diseases
XX CC associated with aberrant hu-Asp1 expression and activity such as
XX CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
XX CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
XX CC sequence represents human amyloid precursor protein APP695-KK, which is
XX CC given in an example from the present invention.

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XX	SQ	Sequence	697 AA;
XX	Qy	Query Match	100.0%; Score 3651; DB 23; Length 697;
XX	Db	Best Local Similarity	100.0%; Pred. No. 1.7e-256;
XX	Db	Matches 697; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRINMHNQVQKWDSPSGTK	60
Db	1	MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRINMHNQVQKWDSPSGTK	60
Qy	61	TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONCKRGRKOCKTHPHEVPIYRCVIG	120
Db	61	TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONCKRGRKOCKTHPHEVPIYRCVIG	120
Qy	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTYAKETCSKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHWHTYAKETCSKSTNLHDYGMLLPCGIDKFR	180
Qy	181	GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEE	240
Qy	241	EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEEYVVRVPTTAASPDVAV	300
Db	241	EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEEYVVRVPTTAASPDVAV	300
Qy	301	DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF	360
Qy	361	QKVESLEQEAANERQOQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK	420
Db	361	QKVESLEQEAANERQOQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYIERMNSLSLLYNPFAVA	480
Db	421	KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYIERMNSLSLLYNPFAVA	480
Qy	481	BEIOPVDELLIOKQNTSYDVLANKWISSEPRISYNDALMPSLTELKTVELLPVNGEFL	540
Db	481	BEIOPVDELLIOKQNTSYDVLANKWISSEPRISYNDALMPSLTELKTVELLPVNGEFL	540
Qy	541	DLQOPWHSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNFKTEHISEVKMDAEF	600
Db	541	DLQOPWHSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNFKTEHISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEEDVGSNGKGAIIIGLMVGCVIATVITVITVLMKKKQYTSIHGV	660
Db	601	RHDSGYEVHHQKLVFFAEEDVGSNGKGAIIIGLMVGCVIATVITVITVLMKKKQYTSIHGV	660
Qy	661	VEVDAAVTPPEERHLSKMQQNGYENPTYKFFQOMQNK	697
Db	661	VEVDAAVTPPEERHLSKMQQNGYENPTYKFFQOMQNK	697

RESULT 8

AA88430

ID AA88430 standard; Protein: 697 AA.

XX AC

XX AC

XX DT 03-AUG-2000 (first entry)

XX DE Human APP695-VF-KK amino acid sequence.

XX KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

XX KW Alzheimer's disease; beta secretase site; APP695-VF-KK.

XX OS Homo sapiens.

XX PN WO200017369-A2.

XX XX

PD	30-MAR-2000.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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Db 421 KYVRAEOKDRQHTLKHFHEHVMVDPKAAQIRSOVMTLRLVYVERMNSLSLYNYPAVA 480
 QY 481 EIIQDEYDELLOKCNYSDDVLANMISEPRISYGNALMPSLTETITVTELLIPYNCEFSL 540
 Db 481 EIIQDEYDELLOKCNYSDDVLANMISEPRISYGNALMPSLTETITVTELLIPYNCEFSL 540
 QY 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTRHSGSLTRKIBELISVKKMAEF 600
 Db 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTRHSGSLTRKIBELISVKKMAEF 600
 QY 601 RHDSSYEVHOKLVFFRAEDVGSNKGALIGLMVGGVVATVITVTLVLMKKQYTSIHGV 660
 Db 601 RHDSSYEVHOKLVFFRAEDVGSNKGALIGLMVGGVVATVITVTLVLMKKQYTSIHGV 660
 QY 661 VEVDAAVTPPERHLSKMQQNGYENPTYKFFEQMNKK 697
 Db 661 VEVDAAVTPPERHLSKMQQNGYENPTYKFFEQMNKK 697

RESULT 9
 AAEL0637
 ID AAEL0637 standard; Protein: 697 AA.
 AC AAEL0637;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.
 KW Human: aspartyl protease 1; Aspl; amyloid precursor protein;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nontropic; neuroprotective;
 KW APP695-VF-KK; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 642 /note= "Wild-type Val substituted with Phe"
 FT
 XX GB2357767-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-0023315.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PRAA) PHARMACIA & UPJOHN CO.
 PI
 PI Bionkowsk; MJ, Gurney M;
 XX
 DR WPI: 2001-444209/48.
 DR N-PSDB: AAD17873.
 XX
 XX Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease.
 XX
 PS Example 8; Page 120-122; 137fp; English.
 XX

CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
 CC Aspl proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Aspl alpha-secretase

CC activity, which in turn is useful for identifying modulators of
 CC hu-Aspl alpha-secretase activity, where modulators that increase
 CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
 CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Aspl proteolytic activity. The present sequence is human amyloid
 CC protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence
 CC is obtained by the addition of two lysine residues (KK motif) at
 CC the C-terminus of APP695-VF isoform which is generated by the London
 CC mutation in APP695, where Val at position 642 is replaced with Phe.
 CC APP695-VF-KK isoform is useful for assaying the beta-secretase
 CC activity of human aspartyl protease 2a (hu-Asp2a) protein.

XX Sequence 697 AA:

Query Match 99.9%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 4e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPDIAFCGRLLNHHMNVQNGKWDSPSGTK 60
 Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPDIAFCGRLLNHHMNVQNGKWDSPSGTK 60
 QY 61 TCIDTKESILQYQCEVYPELQITNVVEANQPVTIQNMCKRGRKQCKTHPHFV-PYRCLVG 120
 Db 61 TCIDTKESILQYQCEVYPELQITNVVEANQPVTIQNMCKRGRKQCKTHPHFV-PYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHHVTHAKETCSKSTNLHDYGMLLPCGDKDKR 180
 Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHHVTHAKETCSKSTNLHDYGMLLPCGDKDKR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEVEE 240
 Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEVEE 240
 QY 241 EADDEDEDEDEVEEAEPEYEATERTTSIATTTTTESEVEEVVVPVTTAASIPDAV 300
 Db 241 EADDEDEDEDEVEEAEPEYEATERTTSIATTTTTESEVEEVVVPVTTAASIPDAV 300
 QY 301 DKYLETGDENEHAHFQKAKERLEAKHRMSQVMREWEAEACAKNPKADKKAVIQHF 360
 Db 301 DKYLETGDENEHAHFQKAKERLEAKHRMSQVMREWEAEAEQAKNPKADKKAVIQHF 360
 QY 361 QEKVESLQEAANEKQQLVETHHAKVEAMLNDRKRLALENYITALQAVPPRPRHVNMLK 420
 Db 361 QEKVESLQEAANEKQQLVETHHAKVEAMLNDRKRLALENYITALQAVPPRPRHVNMLK 420
 QY 421 KYVRAEOKDRQHTLKHFHEHVMVDPKAAQIRSOVMTLRLVYVERMNSLSLYNYPAVA 480
 Db 421 KYVRAEOKDRQHTLKHFHEHVMVDPKAAQIRSOVMTLRLVYVERMNSLSLYNYPAVA 480
 QY 481 FEIQDEYDELLOKCNYSDDVLANMISEPRISYGNALMPSLTETITVTELLIPYNCEFSL 540
 Db 481 FEIQDEYDELLOKCNYSDDVLANMISEPRISYGNALMPSLTETITVTELLIPYNCEFSL 540
 QY 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTRHSGSLTRKIBELISVKKMAEF 600
 Db 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTRHSGSLTRKIBELISVKKMAEF 600
 QY 601 RHDSSYEVHOKLVFFRAEDVGSNKGALIGLMVGGVVATVITVTLVLMKKQYTSIHGV 660
 Db 601 RHDSSYEVHOKLVFFRAEDVGSNKGALIGLMVGGVVATVITVTLVLMKKQYTSIHGV 660
 QY 661 VEVDAAVTPPERHLSKMQQNGYENPTYKFFEQMNKK 697
 Db 661 VEVDAAVTPPERHLSKMQQNGYENPTYKFFEQMNKK 697

RESULT 10
 AAEL06867

AAE06867 standard; Protein; 697 AA.
AAE06867;
23-OCT-2001 (first entry)
Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.
Human: aspartyl protease; Asp: beta-amyloid precursor protein 695-VF-KK;
beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
neuroprotective; antisense therapy; gene therapy; APP695-VF-KK: mutant;
mutin.
Homo sapiens.
OS Synthetic.
XX Key location/Qualifiers
FH Misc-difference 642 /note= "Wild type Val substituted with Phe"
FT W0200150829-A2.
XX 19-JUL-2001.
XX 09-MAY-2001: 2001W0-1B00799.
XX 09-MAY-2001: 2001W0-1B00799.
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (FANR/) YAN R.
XX Hienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI: 2001-483072/52.
XX N-PSDS: AAD13029.
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity -
XX Example 8: Page 150-152: 185pp: English.
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
XX precursor protein (APP) isoforms and their corresponding DNA molecules.
XX Human aspartyl proteases can act as beta-secretase proteases useful for
XX treating Alzheimer's disease. APP isoforms are useful for identifying
XX modulators of amyloid-beta peptide production, for use in designing
XX therapeutics for the treatment and prevention of Alzheimer's disease,
XX dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
XX and neuronal loss. APP isoforms are also used in methods for identifying
XX inhibitors and modulators of human Asp2 activity. The invention relates
XX to a method for identifying agents that modulate the activity of human
XX aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
XX as a means to screen in cellular assays for the inhibitors of beta- and
XX gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
XX polymerase chain reactions (PCR). The probes are useful for detecting
XX Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
XX blots. The present sequence is modified human amyloid precursor
XX protein 695-VF-KK (APP695-VF-KK) isoform. APP695-VF-KK isoform is
XX obtained by addition of two lys residues (KK motif) at the C-terminal
XX end of APP695-VF isoform. APP695-VF isoform is obtained by London V-F
XX mutation in APP695 isoform, where Val at position 642 is replaced with
XX Phe. APP695-VF-KK isoform is useful for assaying the beta-secretase
XX activity of human aspartyl protease 2a (Hu-Asp2a) protein.
XX Sequence 697 AA:
Query Match: 99.9%; Score 3646; DB 22: Length 697;

Best Local Similarity 99.9%; Pred. No. 4e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEQIAMFCGRLNMHMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEQIAMFCGRLNMHMVQNGKWDSPSGTK 60
QY 61 TCIDTKREGILOXCOEYVPELQITNVVEANOPVTIONMCKRGKCKCTHPHFVLPYRCLVG 120
DB 61 TCIDTKREGILOXCOEYVPELQITNVVEANOPVTIONMCKRGKCKCTHPHFVLPYRCLVG 120
QY 121 EFVSODALLVPDKCKFLHQRMDVDCETHLHWHTVAKETSEKSTNLHDYGMJLPCGIDKFR 180
DB 121 EFVSODALLVPDKCKFLHQRMDVDCETHLHWHTVAKETSEKSTNLHDYGMJLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEVAEEVAEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEVAEEVAEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATITTTTTSVEEVVVRVPTTAASPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATITTTTTSVEEVVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRMRMSQVMREWEAEAEQAKNLPKAKKAVIQHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHRMRMSQVMREWEAEAEQAKNLPKAKKAVIQHF 360
QY 361 QEKVESLEQSAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQSAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAFQKDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVYERMNQSLSLYNNPVA 480
DB 421 KYVRAFQKDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVYERMNQSLSLYNNPVA 480
QY 481 EIQDQVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTLTETKTVELLPVNGEFSL 540
DB 481 EIQDQVDELLQKEQNYSDVLANMISEPRISYGNDAIMPSTLTETKTVELLPVNGEFSL 540
QY 541 DLQPMHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTSEISEVKMDAEF 600
DB 541 DLQPMHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTSEISEVKMDAEF 600
QY 601 RHDSGYEVHQQKLVFPFAEDVGSNGKGAIGLMVGCVVIATVIVILVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHQQKLVFPFAEDVGSNGKGAIGLMVGCVVIATVIVILVMKKKQYTSIHGV 660
QY 661 VEYDAAVTPERHLSKMQQNGYENPTYKFEQUMONKK 697
DB 661 VEYDAAVTPERHLSKMQQNGYENPTYKFEQUMONKK 697
AAU06611 standard; Protein: 697 AA.
AC AAU06611;
XX 24-OCT-2001 (first entry)
XX Human: Amyloid precursor protein mutant, APP695-VF-KK.
XX Human: Aspartyl protease; Asp2b; beta-secretase; neurotropic;
XX neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
XX amyloid-beta; Abeta; APP695-VF-KK; London mutant; mutant; mutin.
XX Homo sapiens.
XX Key location/Qualifiers
FH Misc-difference 642 /note= "Wild-type Val substituted by Phe"
FT Misc-difference 696..697
FT Misc-difference /note= "2 Extra Lys residues added compared to

Wild-Type AP2695*

FT WO200149098-A2.
 XX
 XX 12-JUL-2001.

XX 09-MAY-2001; 2001WO-IB00798.
 XX 09-MAY-2001; 2001WO-IB00798.
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
 XX WP1; 2001-502549/55.
 DR N-PSDB; AAS11525.
 XX

XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity

XX Example 8; Page 150-152; 185pp; English.

XX The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp2) protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the APP-SW-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC APP oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-APP nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is the human
 CC APP695 mutant, APP695-VF-KK which has 2 extra Lys residues added at the
 CC C-terminus compared to APP695-VF (the London mutation). The mutation
 CC alters the specificity of the APP gamma-secretase activity and increases
 CC the rate of processing of the amyloid A-beta peptide.

XX Sequence 697 AA;

Query Match 99.98; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.98; Pred. No. 4e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMVQNGKDSDFGK 60
 DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMVQNGKDSDFGK 60
 QY 61 TCIDTKESILQYCEVYPELQITNWVEANOPVTIOWCKRGKQCKTHPHFVTPCLVS 120
 DB 61 TCIDTKESILQYCEVYPELQITNWVEANOPVTIOWCKRGKQCKTHPHFVTPCLVS 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPCGGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPCGGIDKFR 180

QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE 240
 XX
 XX 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE 240
 XX
 XX 241 EADDDDEEDGDEVEAEAEPEEAEETKTSJATTTTITTESVEEVVRYPTTAASIPDAV 300
 XX
 XX 241 EADDDDEEDGDEVEAEAEPEEAEETKTSJATTTTITTESVEEVVRYPTTAASIPDAV 300
 XX
 XX 302 DKYLETGPDENEHAFHOKAKERIEAKHREHMSQVHREWEAEKQAKNLPKADKKAVIOHF 360
 XX
 XX 302 DKYLETGPDENEHAFHOKAKERIEAKHREHMSQVHREWEAEKQAKNLPKADKKAVIOHF 360
 XX
 XX 361 QEKVESLECEANANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 XX
 XX 361 QEKVESLECEANANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 XX
 XX 421 KYVRAEQKDRQHTLKIFEHVRYMVDPKKAAQIRSQVTHLRVIERMNSLSLLYNPVA 480
 XX
 XX 421 KYVRAEQKDRQHTLKIFEHVRYMVDPKKAAQIRSQVTHLRVIERMNSLSLLYNPVA 480
 XX
 XX 481 BEIQDEVDELLOKEQVSDVLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEESL 540
 XX
 XX 481 BEIQDEVDELLOKEQVSDVLANMISEPRI SYGNDALMPSLTETKTTVELLPVNGEESL 540
 XX
 XX 541 DDLQPHWSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKITEISEVKMDA 600
 XX
 XX 541 DDLQPHWSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKITEISEVKMDA 600
 XX
 XX 601 RHDSGYEVHOKLVFAEDVGSNKGALIGLVGGVVIVITLVMLKKOYTSIHGCV 660
 XX
 XX 601 RHDSGYEVHOKLVFAEDVGSNKGALIGLVGGVVIVITLVMLKKOYTSIHGCV 660
 XX
 XX 661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMNKK 697
 XX
 XX 661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMNKK 697
 XX

RESULT 12
 AA007210
 ID AA007210 standard; Protein: 697 AA.
 XX
 XX AA007210;
 XX
 XX 24-OCT-2001 (first entry)
 XX
 XX Human beta-amyloid protein precursor, APP695-VF-KK.
 DE
 XX Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KW beta-secretase; Alzheimer's disease; APP695-VF-KK.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 642
 FT /note= "Wild type Val substituted by Phe"
 XX
 XX WO200149097-A2.
 XX
 XX 12-JUL-2001.
 XX
 XX 09-MAY-2001; 2001WO-IB00797.
 XX
 XX 09-MAY-2001; 2001WO-IB00797.
 XX
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

XX WPI: 2001-502548/55.
 DR N-PSDB: AAS11710.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX
 PS Example 8; Page 150-152; 185pp; English.
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, AP:695-VF-KK,
 CC used in the method of the invention.
 XX
 SQ Sequence 697 AA:

Query Match 99.9%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 4e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

Qy 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPPQIAEMFCGRNLNMMHYQNGKWDSPSGTK 60
 Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPPQIAEMFCGRNLNMMHYQNGKWDSPSGTK 60

Qy 61 TCIDTKGILQYCOEVPPELQITWVVEANQPVTTQNMCKGRKCKTHPIFVPIYRCLVG 120
 Db 61 TCIDTKGILQYCOEVPPELQITWVVEANQPVTTQNMCKGRKCKTHPIFVPIYRCLVG 120

Qy 121 EFVSDALLVPDKCFELHQRNDVCETHLHWHITVAKETCSKSTNLHSDYGMLEPGIDKFR 180
 Db 121 EFVSDALLVPDKCFELHQRNDVCETHLHWHITVAKETCSKSTNLHSDYGMLEPGIDKFR 180

Qy 181 GVERVCCPLAESQNVSDAEDDDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
 Db 181 GVERVCCPLAESQNVSDAEDDDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240

Qy 241 EADDDDEDDGDEVEEAEVEEATERTISIAITTTTTSVEFVVRVPTTASTDPAV 300
 Db 241 EADDDDEDDGDEVEEAEVEEATERTISIAITTTTTSVEFVVRVPTTASTDPAV 300

Qy 301 DKYLETGDENEHAFQKAKERLEAKHREKRSQVMREWEAEERQAKNLPKADKKAVTORF 360
 Db 301 DKYLETGDENEHAFQKAKERLEAKHREKRSQVMREWEAEERQAKNLPKADKKAVTORF 360

Qy 361 QEKVESLEQEANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPREFVNMK 420
 Db 361 QEKVESLEQEANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPREFVNMK 420

Qy 421 KYVRAEQDRQHTLKHFEHVRMVPDKKAAQIRSQVMTHLRIYIERMQNSLLYNPFAVA 480
 Db 421 KYVRAEQDRQHTLKHFEHVRMVPDKKAAQIRSQVMTHLRIYIERMQNSLLYNPFAVA 480

Qy 481 EEIQTQVDELLQKEQNSDDVLANMISFPRISYGNALMPSLTETKTVELLPVNGEFSI 540

Db 481 EEIQTQVDELLQKEQNSDDVLANMISFPRISYGNALMPSLTETKTVELLPVNGEFSI 540
 Qy 541 DDLOPWHSTGADSVPAANTENEPVDARPAADAGLTTRPGSGLTNKTEISEVKMDAEF 600
 Db 541 DDLOPWHSTGADSVPAANTENEPVDARPAADAGLTTRPGSGLTNKTEISEVKMDAEF 600

Qy 601 RHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGGVVIAIVITLVMLKKKQYTSIHGV 660
 Db 601 RHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGGVVIAIVITLVMLKKKQYTSIHGV 660

Qy 661 VEYDAAVTPERHLKSMQNGYENPTYKPFQEQMKNK 697
 Db 661 VEYDAAVTPERHLKSMQNGYENPTYKPFQEQMKNK 697

RESULT 13
 AAE02589
 ID AAE02589 standard; Protein; 697 AA.
 XX AAE02589;
 AC AAE02589;
 XX
 PT 10-AUG-2001 (first entry)
 XX
 DE Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).
 XX
 KW Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;
 KW APP695-VF-KK; Alzheimer's disease; antialzheimer's.
 XX Homo sapiens.
 CS Synthetic.
 XX
 PK WC200123533-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000MO-US26080.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99WC-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PRAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienkowski MJ;
 XX
 DR WPI: 2001-290516/30.
 DR N-PSDB: AAD06747.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease -
 XX
 PS Example 8; Page 149-151; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human APP695-VF-KK. This
 CC sequence is characterised by a V to F alteration at position 642
 CC and contains two carboxy-terminal lysine residues.
 XX
 SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 4e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

Qy 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPPQIAEMFCGRNLNMMHYQNGKWDSPSGTK 60
 Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPPQIAEMFCGRNLNMMHYQNGKWDSPSGTK 60

61 TCIDTREGILOYCOEYVPEQITNVVEANOPVTIONMCKGRKQCKTHPHFVPIYRCVLS 120
 61 TCIDTREGILOYCOEYVPEQITNVVEANOPVTIONMCKGRKQCKTHPHFVPIYRCVLS 120
 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHIVAKETCSKSTNLHDYGMLLPQCTDKFR 180
 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHIVAKETCSKSTNLHDYGMLLPQCTDKFR 180
 181 GVEFVCCPLAESDNVDSADAEEDSDVMGADTDYADGSEKXVVEAEVEAEVEE 240
 181 GVEFVCCPLAESDNVDSADAEEDSDVMGADTDYADGSEKXVVEAEVEAEVEE 240
 241 EADDEDEDGDEVEEAPEEATERTTSIATTTTTTTSVEEVVVPVTTAASTPDV 300
 241 EADDEDEDGDEVEEAPEEATERTTSIATTTTTTTSVEEVVVPVTTAASTPDV 300
 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 361 QEKVESLEOEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 361 QEKVESLEOEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 421 KYVRAECKDRQHTLKHFERVYRWYDPKKAQIRSCVWTHLRVIYERNQSLSLYNVPAVA 460
 421 KYVRAECKDRQHTLKHFERVYRWYDPKKAQIRSCVWTHLRVIYERNQSLSLYNVPAVA 460
 481 EETQDEVELLQEQNYSDIVLANM:SEPRISYGNDAIMPSTLETITVELLPVNGEFSI 540
 481 EETQDEVELLQEQNYSDIVLANM:SEPRISYGNDAIMPSTLETITVELLPVNGEFSI 540
 541 DDLQPHSFGADSVPAANTEVEPVDAARADGLTRPGSGSLTNKIEBEISEVKNDAEF 600
 541 DDLQPHSFGADSVPAANTEVEPVDAARADGLTRPGSGSLTNKIEBEISEVKNDAEF 600
 601 RHDSGVEVHOKLVFAEDVGSNKGALIGLVGSGVVIATVITLVNMLKKQYTSIHGV 660
 601 RHDSGVEVHOKLVFAEDVGSNKGALIGLVGSGVVIATVITLVNMLKKQYTSIHGV 660
 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 14
 ABB78598
 AC ABB78598 standard: Protein: 697 AA.
 AC ABB78598
 UI 16-JUL-2002 (first entry)
 DE Human: APP695-VF-KK protein sequence SEQ ID NO:20.
 KW Human: Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
 KW proteolytic; amyloid precursor protein; App.
 OS Homo sapiens.
 PN GB2367060-A.
 PD 27-MAR-2002.
 XX 29-OCT-2001: 2001GR-0025934.
 PR 23-SEP-1999: 99US-155493P.
 PR 23-SEP-1999: 99WO-0404133.
 PR 13-OCT-1999: 99US-04:6901.
 PR 06-DEC-1999: 99US-162232P.
 PR 22-SEP-2000: 2000GB-0023315.

XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Blenkowski MJ, Gurney M;
 XX
 WP1: 2002-396337/43.
 DR N-PSDB; ABL52465.
 XX
 PT Human aspartyl protease 1 substrates useful in assays to detect
 PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 PT disease
 XX
 PS Example 8: Page 120-122: 182pp; English.
 XX
 CC The present invention describes a human aspartyl protease 1 (hu-Aspl)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Aspl
 CC proteolytic activity, comprising: (a) contacting a hu-Aspl protein with
 CC (1) under acidic conditions; and (b) determining the level of hu-Aspl
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
 CC Aspl proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain); (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Aspl (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III') and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Aspl protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Aspl expression and activity such as
 CC Alzheimer's disease. Hu-Aspl has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents human amyloid precursor protein APP695-VF-KK, which
 CC is given in an example from the present invention.

XX
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 Query Match 99.9%; Score 3646; DB 23; Length 697;
 Best Local Similarity 99.9%; Pred. No. 4e-255;
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 AC AAY88429;
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 DT C3-AUG-2000 (first entry)
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 DE Human APPSW-KK amino acid sequence.
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 KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
 KW Alzheimer's disease; beta secretase site; APPSW-KK.
 XX
 QS Homo sapiens.
 XX
 PN WO200017369-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 23-SEP-1999; 95WO-US20881.
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 PR 24-SEP-1998; 98US-0101594.
 XX
 PA (PhAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan F;
 XX
 DR WPI: 2000-303209/26.
 DR N-PSDB: AAA15666.
 XX
 P: New enzyme designated human aspartase useful in research into
 P: Alzheimer's Disease is capable of cleaving amyloid protein precursor at
 P: the beta secretase site to produce amyloid beta peptide -
 XX
 PS Claim 133; Page 143-147; 183pp; English.
 XX

This sequence represents a modified version of the human amyloid precursor protein (APP) amino acid sequence. The sequence is used in an example of the method of the invention, to show that modification of APP increases beta amyloid protein processing. The invention relates to a protease (e.g. Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DSG or DTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the

CC methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.
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 Best Local Similarity 99.7%; Pred. No. 6.6e-256;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 14:00:39 : Search time 39 Seconds
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Title: US-09-806-194-16

Perfect score: 3651

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Searched: 587654 seqs, 15812981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3651	100.0	697	9	US-09-794-743-16 Sequence 16, Appl
4	3651	100.0	697	9	US-09-794-748-16 Sequence 16, Appl
5	3651	100.0	697	9	US-09-794-925-16 Sequence 16, Appl
6	3651	100.0	697	9	US-09-681-442-16 Sequence 16, Appl
7	3651	100.0	697	11	US-09-869-414-16 Sequence 16, Appl
8	3651	100.0	697	11	US-09-548-366-16 Sequence 16, Appl
9	3646	99.9	697	9	US-09-794-927-20 Sequence 20, Appl
10	3646	99.9	697	9	US-09-795-847-20 Sequence 20, Appl
11	3646	99.9	697	9	US-09-794-743-20 Sequence 20, Appl
12	3646	99.9	697	9	US-09-794-748-20 Sequence 20, Appl
13	3646	99.9	697	9	US-09-794-925-20 Sequence 20, Appl
14	3646	99.9	697	9	US-09-681-442-20 Sequence 20, Appl
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16	3646	99.9	697	11	US-09-548-366-20	Sequence 20, Appl
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21	3643	99.8	697	9	US-09-794-925-18	Sequence 18, Appl
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23	3643	99.8	697	11	US-09-869-414-18	Sequence 18, Appl
24	3643	99.8	697	11	US-09-548-366-18	Sequence 18, Appl
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ALIGNMENTS

RESULT :

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; Sequence 16, Application US/09794927
; Patent No. US20010018324A
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Van, Riquang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, ADP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: US95
: FILE REFERENCE: 28341/6280DE
: CURRENT APPLICATION NUMBER: US/09/795,847
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/-55,493
: PRIOR FILING DATE: 1999-09-23
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: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
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: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-795-847-16

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Best Local Similarity 100.0%; Pred. No. 1,1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang

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; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1,1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLPGLALLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNHMNVQNGKWDSPGSGTK 60
Db 1 MLPGLALLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNHMNVQNGKWDSPGSGTK 60
Qy 61 TCIDTKESILQYCEVYPELQITNVVEANQPVTIONNCKRGRKOCKTHPHFVPIYRCVLG 120
Db 61 TCIDTKESILQYCEVYPELQITNVVEANQPVTIONNCKRGRKOCKTHPHFVPIYRCVLG 120
Qy 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGGIDKFR 180
Qy 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEVAEVEE 240
Qy 241 EADDEDEDEGDEVEEAEPEYEATERTTISIATTTTTTSTESVEEVVPTTAASTPDV 300
Db 241 EADDEDEDEGDEVEEAEPEYEATERTTISIATTTTTTSTESVEEVVPTTAASTPDV 300
Qy 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Qy 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSOVMTHLVRVIERMQSLSLLYNPAVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSOVMTHLVRVIERMQSLSLLYNPAVA 480
Qy 661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMNKK 697

Db 661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMNKK 697

RESULT 4

US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1,1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLPGLALLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNHMNVQNGKWDSPGSGTK 60
Db 1 MLPGLALLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNHMNVQNGKWDSPGSGTK 60
Qy 61 TCIDTKESILQYCEVYPELQITNVVEANQPVTIONNCKRGRKOCKTHPHFVPIYRCVLG 120
Db 61 TCIDTKESILQYCEVYPELQITNVVEANQPVTIONNCKRGRKOCKTHPHFVPIYRCVLG 120
Qy 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGGIDKFR 180
Qy 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEVAEVEE 240
Qy 241 EADDEDEDEGDEVEEAEPEYEATERTTISIATTTTTTSTESVEEVVPTTAASTPDV 300
Db 241 EADDEDEDEGDEVEEAEPEYEATERTTISIATTTTTTSTESVEEVVPTTAASTPDV 300
Qy 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Qy 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSOVMTHLVRVIERMQSLSLLYNPAVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSOVMTHLVRVIERMQSLSLLYNPAVA 480

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QY 481 EEIQDEVDLQKEQNSDVLANKISEPRISYGNDA:MPSLTETKTIVELLVNGEFSL 540
DB 481 EEIQDEVDLQKEQNSDVLANKISEPRISYGNDA:MPSLTETKTIVELLVNGEFSL 540
QY 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSGLTNKTIFEISEVKMDAEF 600
DB 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSGLTNKTIFEISEVKMDAEF 600
QY 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGCVVIATVITLVM:KKKQYTSIHIGV 560
DB 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGCVVIATVITLVM:KKKQYTSIHIGV 560
QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 597
DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 597

RESULT 5
US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280H
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20681
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.le-225;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNHMNVQNGKWSDDPSGK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNHMNVQNGKWSDDPSGK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGRKCKTHPHFVTPYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGRKCKTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETQSKSTNLHDYGMLLPCGGDKXER 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETQSKSTNLHDYGMLLPCGGDKXER 180
QY 181 GVEFVCCPLAESDNVDSADAEEDDDSVMMGGADTDYADGSEKXVVEAEAEAEVAEVEFE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDDDSVMMGGADTDYADGSEKXVVEAEAEAEVAEVEFE 240
QY 241 EADDEDEDEGDEVEEAEPEEATERTTIS:ATTTTTTESVEEVVVRPTTAASTPDAY 300
DB 241 EADDEDEDEGDEVEEAEPEEATERTTIS:ATTTTTTESVEEVVVRPTTAASTPDAY 300
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DB 241 EADDEDEDEGDEVEEAEPEEATERTTIS:ATTTTTTESVEEVVVRPTTAASTPDAY 300
QY 301 DKYLETPDGENEHAIFOKAKERLEAKHRERMSQVNRWEAEARQAKNLPRADKKAV:QHF 360
DB 301 DKYLETPDGENEHAIFOKAKERLEAKHRERMSQVNRWEAEARQAKNLPRADKKAV:QHF 360
QY 361 QFKVESLSEAEANRQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNKIK 420
DB 361 QFKVESLSEAEANRQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNKIK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMDPKKAAQIRSOVMTHLRVIYERMNQS:SLLYNPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMDPKKAAQIRSOVMTHLRVIYERMNQS:SLLYNPAVA 480
QY 481 EEIQDEVDLQKEQNSDVLANKISEPRISYGNDA:MPSLTETKTIVELLVNGEFSL 540
DB 481 EEIQDEVDLQKEQNSDVLANKISEPRISYGNDA:MPSLTETKTIVELLVNGEFSL 540
QY 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSGLTNKTIFEISEVKMDAEF 600
DB 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSGLTNKTIFEISEVKMDAEF 600
QY 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGCVVIATVITLVM:KKKQYTSIHIGV 560
DB 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGCVVIATVITLVM:KKKQYTSIHIGV 560
QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 597
DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 597

RESULT 6
US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20681
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.le-225;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNHMNVQNGKWSDDPSGK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNHMNVQNGKWSDDPSGK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGRKCKTHPHFVTPYRCLVG 120
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Db      61  TCIDTKEGILQYCEVYPELQITNNVEANQPTVQNMCKRGKQCKTHPRFVIPYRCLVG 120
QY      121  EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCEKSTNLDYGNLPLCKGIDKFR 180
Db      122  EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCEKSTNLDYGNLPLCKGIDKFR 180
QY      181  GVEFVCCPLAESUNVDSADAEDSDVWVGADTDYADGSDCKVVEVAEEVEEVEE 240
Db      181  GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSDCKVVEVAEEVEEVEE 240
QY      241  EADDDDEDDGDEVEEAEPEYEBATERTTSTATTTTTTSTESVEEVVRVPTAASTPDV 300
Db      241  EADDDDEDDGDEVEEAEPEYEBATERTTSTATTTTTTSTESVEEVVRVPTAASTPDV 300
QY      301  DKYLETPGDENHAHFQKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
Db      301  DKYLETPGDENHAHFQKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY      361  QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
Db      361  QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY      421  KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
Db      421  KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
QY      481  EIQDEVDLLOKQKONYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFS 540
Db      481  EIQDEVDLLOKQKONYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFS 540
QY      541  DLQPHWSFGADSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTFEISEVKMDAEF 600
Db      541  DLQPHWSFGADSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTFEISEVKMDAEF 600
QY      601  RHDGSEYVHHOKLVFEAEVDGSKNGAIIGLVGGVVIATVITVLMLKKKQYTSIHGV 660
Db      601  RHDGSEYVHHOKLVFEAEVDGSKNGAIIGLVGGVVIATVITVLMLKKKQYTSIHGV 660
QY      661  VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
Db      661  VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 7
US-09-869-414-16
: Sequence 16, Application US/09369414
: Publication No. US2003007226A1
: GENERAL INFORMATION:
: APPLICANT: Beinowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
: FILE REFERENCE: 28342/6280M
: CURRENT FILING DATE: 2001-06-27
: PRIOR FILING DATE: 09/416,901
: PRIOR FILING DATE: 1998-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-869-414-16
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Query Match      100.0%; Score 3651; DB 11; Length 697;
Best Local Similarity 100.0%; Pred. No. 1,1c-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLPGLALLLLAAWTAARALEVPTDGNAGLLAPQIAFMFCGRLLNMHMNVONGKWDSDPSG 60
Db      1  MLPGLALLLLAAWTAARALEVPTDGNAGLLAPQIAFMFCGRLLNMHMNVONGKWDSDPSG 60
QY      61  TCIDTKEGILQYCEVYPELQITNNVEANQPTVQNMCKRGKQCKTHPRFVIPYRCLVG 120
Db      61  TCIDTKEGILQYCEVYPELQITNNVEANQPTVQNMCKRGKQCKTHPRFVIPYRCLVG 120
QY      121  EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCEKSTNLDYGNLPLCKGIDKFR 180
Db      121  EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCEKSTNLDYGNLPLCKGIDKFR 180
QY      181  GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSDCKVVEVAEEVEEVEE 240
Db      181  GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSDCKVVEVAEEVEEVEE 240
QY      241  EADDDDEDDGDEVEEAEPEYEBATERTTSTATTTTTTSTESVEEVVRVPTAASTPDV 300
Db      241  EADDDDEDDGDEVEEAEPEYEBATERTTSTATTTTTTSTESVEEVVRVPTAASTPDV 300
QY      301  DKYLETPGDENHAHFQKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
Db      301  DKYLETPGDENHAHFQKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY      361  QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
Db      361  QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY      421  KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
Db      421  KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
QY      481  EIQDEVDLLOKQKONYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFS 540
Db      481  EIQDEVDLLOKQKONYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFS 540
QY      541  DLQPHWSFGADSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTFEISEVKMDAEF 600
Db      541  DLQPHWSFGADSVPANTENEVEPVDARPAADRGLTTRPGSLTNIKTFEISEVKMDAEF 600
QY      601  RHDGSEYVHHOKLVFEAEVDGSKNGAIIGLVGGVVIATVITVLMLKKKQYTSIHGV 660
Db      601  RHDGSEYVHHOKLVFEAEVDGSKNGAIIGLVGGVVIATVITVLMLKKKQYTSIHGV 660
QY      661  VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
Db      661  VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 8
US-09-548-366-16
: Sequence 16, Application US/09548366
: Publication No. US20030104365A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
: TITLE OF INVENTION: USES THEREFOR
: FILE REFERENCE: 28341/6280A
: CURRENT APPLICATION NUMBER: US/09/548,366
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
us-09-348-366-16

Query Match
Best Local Similarity 100.0%; Score 3651; DB 11; Length 697;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MLPLGALLLLAANTARALEVPTDGNAGLLAEPIQIAFMCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPIQIAFMCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTREGILQYQCVYPELOITNVVEANQPTVIONWCKRGKCKCTHPIHFVYPCVLG 120
DB 61 TCIDTREGILQYQCVYPELOITNVVEANQPTVIONWCKRGKCKCTHPIHFVYPCVLG 120
QY 121 EFVSDALLVPDKCKFQHGERMDVCETHLHHHTVAKETSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFQHGERMDVCETHLHHHTVAKETSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
DB 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNMLK 420
QY 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
DB 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
QY 481 EPIQDEVDELLOKEQYSDVLANMISEPRIISYGNDAIMPSTETKTITVELLPVNGEFS 540
DB 481 EPIQDEVDELLOKEQYSDVLANMISEPRIISYGNDAIMPSTETKTITVELLPVNGEFS 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEYDAAVTPERHLKMQQNGYENPTYKFEQMNKK 697
DB 661 VEYDAAVTPERHLKMQQNGYENPTYKFEQMNKK 697
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RESULT 9

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us-09-794-927-20
; Sequence 20, Application: us/09794927
; Patent No. US20010016324a1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michae. J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
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; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: CSES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/415,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
us-09-794-927-20
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Query Match 99.9%; Score 3646; DB 9; Length 697;

Best Local Similarity 99.9%; Pred. No. 2.2e-225;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPIQIAFMCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPIQIAFMCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTREGILQYQCVYPELOITNVVEANQPTVIONWCKRGKCKCTHPIHFVYPCVLG 120
DB 61 TCIDTREGILQYQCVYPELOITNVVEANQPTVIONWCKRGKCKCTHPIHFVYPCVLG 120
QY 121 EFVSDALLVPDKCKFQHGERMDVCETHLHHHTVAKETSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFQHGERMDVCETHLHHHTVAKETSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
DB 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNMLK 420
QY 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
DB 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
QY 481 EPIQDEVDELLOKEQYSDVLANMISEPRIISYGNDAIMPSTETKTITVELLPVNGEFS 540
DB 481 EPIQDEVDELLOKEQYSDVLANMISEPRIISYGNDAIMPSTETKTITVELLPVNGEFS 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
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QY 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQMKNK 697
 DB 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQMKNK 697

RESULT 10

US-09-795-847-20
 : Sequence 20, Application US/09795847
 : Patent No. US20010018208A1
 : GENERAL INFORMATION:
 : APPLICANT: Gurney, Mark E.
 : APPLICANT: Bienkowski, Michael J.
 : APPLICANT: Heinrichson, Robert L.
 : APPLICANT: Parodi, Luis A.
 : APPLICANT: Yan, Riqiang
 : TITLE OF INVENTION: ALZHEIMER'S D-SEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 : TITLE OF INVENTION: USES
 : TITLE OF INVENTION: THEREFOR
 : FILE REFERENCE: 28341/6280DE
 : CURRENT APPLICATION NUMBER: US/09/795.847
 : PRIOR FILING DATE: 2001-02-28
 : PRIOR APPLICATION NUMBER: 09/416,901
 : PRIOR FILING DATE: 1999-10-13
 : PRIOR APPLICATION NUMBER: 60/155,493
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: 09/404,133
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: PCT/US99/20881
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: 60/101,594
 : PRIOR FILING DATE: 1998-09-24
 : NUMBER OF SEQ ID NOS: 73
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 20
 : LENGTH: 697
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-795-847-20

Query Match 99.9% Score 3646; DB 9; Length 697;
 Best Local Similarity 99.9% Pred. No. 2.2e-225;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHMNVQNGKWDSPSGIK 60
 DB 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHMNVQNGKWDSPSGIK 60
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 DB 61 TCIDTKESILQYCOEYVPELOITNVVEANQPVTTQNKCKRGKCKKTHPHFVPIYRCVLG 120
 QY 121 EFVSDALLVPCKKFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
 DB 121 EFVSDALLVPCKKFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240
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 DB 241 FADDDDEDDGDEVEEAEPEYEATERTTSIATITTTTSTVESVEWVPTTAASTPDV 300
 QY 301 KYLETPTGDENAHFQAKERLEAKHREMSQVNMREWEAEERQAKNLPKADKKAIVIQIF 360
 DB 301 KYLETPTGDENAHFQAKERLEAKHREMSQVNMREWEAEERQAKNLPKADKKAIVIQIF 360
 QY 361 QEKVLSLEQAEANERQQLVETHMARVEAMLNDRRLALENITALQAVPPRRHVFENMLK 420
 DB 361 QEKVLSLEQAEANERQQLVETHMARVEAMLNDRRLALENITALQAVPPRRHVFENMLK 420
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DB 421 KYVRAEQDKRQHTLKHFEHVRWDPKKAQIRSOVMTHLRYIERMNQSLSLYNPAPA 480
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 DB 481 EIQDEYDELLQKEQNYSDJVLANNMISEPRISYNDALMPSLTETKTTVELLPVNGEFSL 540
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 DB 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
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 DB 601 RHDGSYEVHHQKLVFFAEDVGSNKGAIIGLMWGVWIAIVITVLMKKKQYTSIHGV 660
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 DB 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQMKNK 697

RESULT 11

US-09-794-743-20
 : Sequence 20, Application US/09794743
 : Patent No. US20010021391A1
 : GENERAL INFORMATION:
 : APPLICANT: Gurney, Mark E.
 : APPLICANT: Bienkowski, Michael J.
 : APPLICANT: Heinrichson, Robert L.
 : APPLICANT: Parodi, Luis A.
 : APPLICANT: Yan, Riqiang
 : TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
 : TITLE OF INVENTION: USES
 : TITLE OF INVENTION: THEREFOR
 : FILE REFERENCE: 28341/6280BC
 : CURRENT APPLICATION NUMBER: US/09/794.743
 : PRIOR FILING DATE: 2001-02-27
 : PRIOR APPLICATION NUMBER: 09/416,901
 : PRIOR FILING DATE: 1999-10-13
 : PRIOR APPLICATION NUMBER: 60/155,493
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: 09/404,133
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: PCT/US99/20881
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: 60/101,594
 : PRIOR FILING DATE: 1998-09-24
 : NUMBER OF SEQ ID NOS: 73
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 20
 : LENGTH: 697
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-794-743-20

Query Match 99.9% Score 3646; DB 9; Length 697;
 Best Local Similarity 99.9% Pred. No. 2.2e-225;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHMNVQNGKWDSPSGIK 60
 DB 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHMNVQNGKWDSPSGIK 60
 QY 61 TCIDTKESILQYCOEYVPELOITNVVEANQPVTTQNKCKRGKCKKTHPHFVPIYRCVLG 120
 DB 61 TCIDTKESILQYCOEYVPELOITNVVEANQPVTTQNKCKRGKCKKTHPHFVPIYRCVLG 120
 QY 121 EFVSDALLVPCKKFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
 DB 121 EFVSDALLVPCKKFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-20

Query Match      99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYNONGKWDSDPSGK 60
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DB 61 TCIDTKEGILQYCCQEVYPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
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QY 241 EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTTSVEEVVVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTTSVEEVVVRVPTTAASTPDV 300
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DB 361 QEKVESLEQEAANEKQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNK 420
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DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMKNOSLSLYNVPAVA 480
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DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697

RESULT 14
US-09-681-442-20
; Sequence 20, Application US/09581442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heiorikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280fg
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; CURRENT APPLICATION NUMBER: US/09/681.442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 05/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 05/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-20
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Query Match      99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
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DB 181 GVEFVCCPLAEESNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTTSVEEVVVRVPTTAASTPDV 300
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DB 301 DKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERCAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEKQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNK 420
DB 361 QEKVESLEQEAANEKQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNK 420
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DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697
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RESULT 15

US-09-869-414-20
: Sequence 20, Application US/09869414
: Publication No. US20030077226A1
: GENERAL INFORMATION:
: APPLICANT: Belinkowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
: FILE REFERENCE: 28341/6280M
: CURRENT APPLICATION NUMBER: US/09/869,414
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 66/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2. C
: SEQ ID NO 20
: LENGTH: 697
: TYPE: CPT
: ORGANISM: Homo sapiens
US-09-869-414-20

Query Match: 99.9%; Score 3646; DB 11; Length 697;
Best Local Similarity 99.9%; Pred. No. 2,2e-225;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MLPGLALLLAATARALEVPTDGNAGLLAEPQIAFCGRINMHMNVQNKWSDSPSGTK 60
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DB 121 EFVSDALLVPDKCFLEHQMMDVCETHLHMTVAKECTCEKSTNLHDYGMLLPCGIDKFR 180
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DB 181 GVEFVCCPLAESDNVDSADAEEDSDSVWNGGADTDYADGSEDKVVEVAEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTVSIATITTTTTSVEEVVVPVPTTAASTPDVAV 300
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DB 361 QKVESLSEAEANERQQLVETMARVEAMLNDRRLALENYITALQAVPPRPHVFNCK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQ:RSQVMTHLRVYIERMNSLSLLYNVPAVA 480
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DB 661 VEYDAAVTPPEERHLSKMOONGYENPTYKFFEQMONKK 697

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Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:04 : Search time 16.6667 seconds
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4021.774 Million cell updates/sec

Title: US-09-806-194-16

Perfect score: 3651

Sequence: 1 MLPGLALLLAATARALEV.....QQNGYENPTYKFFEQMUNKK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3641	99.7	695	1 A49795	Alzheimer's disease
2	3590.5	98.3	770	1 QRHUA4	Alzheimer's disease
3	3544	97.1	695	2 S00550	Alzheimer's disease
4	3519	96.4	695	2 A27485	Alzheimer's disease
5	3103	85.0	747	2 JH0773	Alzheimer's disease
6	2105	57.7	484	4 A32761	hypothetical Alzhe
7	1728	47.3	763	2 A49321	amyloid beta (A4)
8	1716	47.0	765	2 S42880	amyloid precursor-
9	1704	46.7	751	2 A49974	beta-amyloid precu
10	1185	32.5	653	2 A46362	amyloid precursor-
11	1143	31.3	511	2 JC1404	CDSEI-box DNA-bind
12	817.5	22.4	686	2 T15795	hypothetical prote
13	747	20.5	886	2 A32758	beta-amyloid-like
14	706	19.3	246	2 S38344	CDSEI-binding prote
15	411	11.3	82	2 PQ0438	Alzheimer's disease
16	296.5	9.1	191	2 A35981	sperm membrane pro
17	283	7.8	57	2 E50045	Alzheimer's disease
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23	217	5.9	42	2 P80512	beta-amyloid prote
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25	186	5.1	5170	2 T15348	hypothetical prote
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27	185.5	5.1	993	2 S49461	synaptonemal compl
28	182	5.0	522	2 I32444	hypothetical prote
29	175.5	4.8	802	1 S48529	NAB3 protein - yea

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microtubule bindin
hypothetical prote
150K golgi antigen
caldesmon-related p
caldesmon - human
h-caldesmon - chis
neurofilament trip
myelin transcript1
glutamate rich pro
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tropoin I, cardia
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transcription fact
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174 4.8 1087 2 T30330
173.5 4.8 793 1 JH0628
172 4.7 771 1 A33430
172 4.7 784 2 P80009
172 4.7 1182 2 T30189
171 4.7 1271 2 A45555
170 4.7 1948 2 S00485
169.5 4.6 298 1 TP0UTC
169.5 4.6 721 2 S29795
169 4.6 885 2 G71608
169 4.6 1187 2 T46637
168.5 4.6 675 2 T03744

ALIGNMENTS

RESULT 1
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Tolan, D.R.; Seikoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human suppo
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote
C:Keywords: alternative splicing

Query Match 99.7%; Score 3641; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 1 MLPGLALLLAATARALEVPTDGNAGLIAEPQIAEFCGRLLMHNVQNGKWDSDPSGK 60
Db 1 MLPGLALLLAATARALEVPTDGNAGLIAEPQIAEFCGRLLMHNVQNGKWDSDPSGK 60
Qy 61 TCIDTKEGILCYCOEYVPELOITNVVEANOPVTIONCKRGRKOCKTTPHFVTPYRCLVG 120
Db 61 TCIDTKEGILCYCOEYVPELOITNVVEANOPVTIONCKRGRKOCKTTPHFVTPYRCLVG 120
Qy 121 EFVSDALLVPKCKFLHQRMDVCETHLHWHIVAKELCSEKSTNLHYGMLLPGGIDKFR 160
Db 121 EFVSDALLVPKCKFLHQRMDVCETHLHWHIVAKELCSEKSTNLHYGMLLPGGIDKFR 160
Qy 181 GVEFVCCPLAFESDNVDSADAEDDDSDVMWGGADTDYADGSEDKVFEVVEEVEEVEE 240
Db 181 GVEFVCCPLAFESDNVDSADAEDDDSDVMWGGADTDYADGSEDKVFEVVEEVEEVEE 240
Qy 241 EADDDEDDGDEVEEFAEPEYEATERITSIATTTTTSVEEYVVRVPTTAASTPDV 300
Db 241 EADDDEDDGDEVEEFAEPEYEATERITSIATTTTTSVEEYVVRVPTTAASTPDV 300
Qy 301 DKYLETPGDENEHAHFOKAKERLEAKRHRMSQVMREWEAEERQAKNLPADKAKVIOHF 360
Db 301 DKYLETPGDENEHAHFOKAKERLEAKRHRMSQVMREWEAEERQAKNLPADKAKVIOHF 360
Qy 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEQKQHTLKHFEHVRMVDPKAAQITRSQVMTHLRVIYERMNOSLLLYNPAVA 480
Db 421 KYVRAEQKQHTLKHFEHVRMVDPKAAQITRSQVMTHLRVIYERMNOSLLLYNPAVA 480

Db 421 KYVRAEQKORHTLKFEHVRWDPKKAQIRSQVTHLRVIYERNQSLSLIYNVPAVA 480
 QY 481 EEIQDEVDELLOKEQNYSDVLANMISEPRI SYGNDALMPSITEIKTTVELLPVNGEFSL 540
 Db 481 EEIQDEVDELLOKEQNYSDVLANMISEPRI SYGNDALMPSITEIKTTVELLPVNGEFSL 540
 QY 541 DDLOPHSHSGAUSVPANTENEPVDARPAADRGLTTRPGSGSLTNKIKTEISEVKNDAEP 600
 Db 541 DDLOPHSHSGAUSVPANTENEPVDARPAADRGLTTRPGSGSLTNKIKTEISEVKNDAEP 600
 QY 601 RHDSGVEVHHQKLVFFAEDYGSNKGAIIGLMWGGVVIAIVIVITLMLKKKYTSIHHCV 660
 Db 601 RHDSGVEVHHQKLVFFAEDYGSNKGAIIGLMWGGVVIAIVIVITLMLKKKYTSIHHCV 660
 QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFEFQMCN 695
 Db 661 VEYDAAVTPEERHLSKMQONGYENPTYKFEFQMCN 695
 RESULT 2
 ORCUA4
 Alzheimer's disease amyloid beta protein precursor (validated) - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xia inhibitor
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
 C:Accession: S05194; A32277; A33260; A35426; 130451; 130453; 159562; A44017
 4668; A28583; A29302; A60805; J00036; S06121; A60355; A59011; A38364; S25076; S98322; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayre, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PrA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by
 A:Reference number: S02260; MUID:89128427; PMID:2783775
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13456
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL data Library, November 1983
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:q871360
 A:Note: alternative splice form APP(695)
 R:LaFauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-protein
 A:Reference number: A32277; MUID:89165870; PMID:2538123
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GR:M24546; GB:M24547; NID:q341202; PIDN:AAQ13054.1; PID:q556074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity
 A:Reference number: A33260; MUID:89392030; PMID:2675937
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 655-737 <JOH>
 A:Cross-references: GR:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244; PMID:2196678
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikawa, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: 139451; MUID:90236318; PMID:2110105
 A:Accession: 139452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:q178613; PIDN:AA859502.1; PID:q178616
 A:Accession: 139451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from
 A:Molecule type: DNA
 A:Residues: 1-530, 'QMLMPVPAFWAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AA859501.1; PID:q178615
 R:Yoshikawa, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference 139451
 R:Levy, P.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral h
 A:Reference number: 139453; MUID:90260663; PMID:2111584
 A:Accession: 139453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Al
 A:Reference number: 159562; MUID:90222553; PMID:1925564
 A:Accession: 159562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AA819991.1; PID:q236721
 R:Kakino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; And
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; M
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds fo
 A:Reference number: A44017; MUID:93035397; PMID:1415269
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:q257377; PIDN:AA823645.1; PID:q257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBI:P:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AA823646.1; PID:q257380
 A:Experimental source: familial Alzheimer disease family LT
 A:Note: sequence extracted from NCBI backbone (NCBI:P:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik,
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-
 A:Reference number: A03134; MUID:87144572; PMID:2881207
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00284; NID:q28525; PIDN:CAA68374.1; PID:q28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovasc
 A:Reference number: A29030; MUID:87231971; PMID:3035574
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AAA51722.1; PID:q178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:38312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R:Schubert, D.; Schroeder, R.; LeCorbier, M.; Saitoh, I.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:38264430; PMID:2968552
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation: copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1573681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <FOI>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase inhibitor
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase inhibitor
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane *status predicted <TM>

Query Match 97.1%; Score 3544; DB 2: Length 695;
Best Local Similarity 97.3%; Pred. No. 5e-179;
Matches 676; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MLPGALLLAATWATRALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60
DB 1 MLPSALLLAATWATRALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCEVYPELQITNVVEANQPTIQNCKRGRKQCKTHPHFVPIPRCLVG 120
DB 61 TCIGTKEGILQYCEVYPELQITNVVEANQPTIQNCKRGRKQCKTHPHFVPIPRCLVG 120

QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180

QY 181 GVEFVCCPLAESDSNVSDAEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDSNVSDAEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

QY 241 EADDEDEDGDEVEEAEPEEATERTTSTATTITTESVEEYVRPTTAASTPDVAV 300
DB 241 EADDEDEDGDEVEEAEPEEATERTTSTATTITTESVEEYVRPTTAASTPDVAV 300

QY 301 DKYLETPGNEHAHQKAKERLEAKHREMSQVREWEAEQAQNLKADKAVIQHF 360
DB 301 DKYLETPGNEHAHQKAKERLEAKHREMSQVREWEAEQAQNLKADKAVIQHF 360

QY 361 OEKVESLEQEAANERQOLVETIHARVEAMLNDRRLALENYITALQAVPRPRHVNMLK 420
DB 361 OEKVESLEQEAANERQOLVETIHARVEAMLNDRRLALENYITALQAVPRPRHVNMLK 420

QY 421 KYVRAEQKQKQHTLKHFEHVRMYDPKKAQKIRSQVNTHLRYIYERNQSLSLCYKVPVAV 480
DB 421 KYVRAEQKQKQHTLKHFEHVRMYDPKKAQKIRSQVNTHLRYIYERNQSLSLCYKVPVAV 480

QY 481 EETQDEVDLLOKEQYSDVLANMISEPRI SYGNDALMPS:TEYKTTVELLPVNGHPSL 540
DB 481 EETQDEVDLLOKEQYSDVLANMISEPRI SYGNDALMPS:TEYKTTVELLPVNGHPSL 540

QY 541 DDLQPMHSFGADSVPAANTENVEPVDARPAADRGLTTRPGSGLTNIKITEISEVKMDAEF 600
DB 541 DDLQPMHSFGADSVPAANTENVEPVDARPAADRGLTTRPGSGLTNIKITEISEVKMDAEF 600

QY 601 RHDSCSYVHHOKLVFFAEDVGSNGKAIIGLMVGVIATVITLVMLKKQYISIHGV 660
DB 601 RHDSCSYVHHOKLVFFAEDVGSNGKAIIGLMVGVIATVITLVMLKKQYISIHGV 660

QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMN 695
DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMN 695

RESULT 4
A27485
A:Title: Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
A:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein.
A:Reference number: A27485; MUID:86106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M.8373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR
A:Cross-references: EMBL:X59379
R:Zimml, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzhe
A:Reference number: I49485; MUID:92203998; PMID:1555768
A:Accession: I49485
A:Status: translated from GB/ENBL/2DRJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type protei
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 96.4%; Score 3519; DB 2: Length 695;
Best Local Similarity 96.8%; Pred. No. 1e-177;
Matches 673; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MLPGALLLAATWATRALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60
DB 1 MLPSALLLAATWATRALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCEVYPELQITNVVEANQPTIQNCKRGRKQCKTHPHFVPIPRCLVG 120
DB 61 TCIGTKEGILQYCEVYPELQITNVVEANQPTIQNCKRGRKQCKTHPHFVPIPRCLVG 120

QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180

QY 181 GVEFVCCPLAESDSNVSDAEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDSNVSDAEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

QY 241 EADDEDEDGDEVEEAEPEEATERTTSTATTITTESVEEYVRPTTAASTPDVAV 300

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Db 241 EADDDDEVDGDEVEEAEAPYEAEATERTTSIATTTTTTIESVEEVVRVPTTAASITDVA 400
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIOHF 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QKVESLEQZAAENRQOLVETIHARVEMLNDRRLALENYITALQAVPRPRHIVENMLK 420
Db 361 QKVESLEQZAAENRQOLVETIHARVEMLNDRRLALENYITALQAVPRPRHIVENMLK 420
QY 421 KYVRAEQKDRHKLKHFHEHVMYDPPKAAQIRSOVMTHLRVIERMNSQLLYNYPAVA 480
Db 421 KYVRAEQKDRHKLKHFHEHVMYDPPKAAQIRSOVMTHLRVIERMNSQLLYNYPAVA 480
QY 481 EETQDEVDLLOKEQNYSDOVLNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Db 481 EETQDEVDLLOKEQNYSDOVLNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDLQPHSFSGADSVPAANTEVEPVDARPAADRGLTTRPGSGLTNKTETSEIYKVKHDAEF 600
Db 541 DDLQPHSFSGADSVPAANTEVEPVDARPAADRGLTTRPGSGLTNKTETSEIYKVKHDAEF 600
QY 601 RHDSGYEVHQRKLVFFAEDVGSNKGAIIGLMVGGVVIATVITLVMLKKKQVTSIHGV 660
Db 601 RHDSGYEVHQRKLVFFAEDVGSNKGAIIGLMVGGVVIATVITLVMLKKKQVTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFEQMON 695
Db 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFEQMON 695

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MGID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PID:AAE24853.1; PID:g26315;
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein: animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 85.08; Score 3103; DB 2; Length 747;
Best Local Similarity 81.08; Pred. No. 8.3e-156;
Matches 598; Conservative 35; Mismatches 41; Indels 64; Gaps 5;

QY 17 ALEYPTDGNAGLLAEPOIAMF-CRLNMHNVQNGKDSPPSGTKTIDTKESGLQVQCE 75
Db 15 ALEYLVDPNGSLLAEPOIAMFVARLNMHNVQNGKWTDSG---CIGTKESGLQVQCE 71
QY 76 VYPELQ-TNNVVEANQPTVIONMCKRGKCKTTHPHFVPIYRCVLGVFVS DALLVPDKCKF 135
Db 72 VYPELQITNNVVEANQPTVIONMCKRGKCKTTHPHFVPIYRCVLGVFVS DALLVPDKCKF 131
QY 136 LQERMOVCFTHLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDND 195
Db 132 LQERMDICTE*HLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDND 191
QY 196 VDSADAEEDSDVMWGADTDYADGSEDKVVEAEVEEAEAEAEAEAEAEAEAEAEAEAE 253
Db 192 FDSADAEEDSDVMWGADTDYADGSEDKVVEAEVEEAEAEAEAEAEAEAEAEAEAEAE 249
QY 254 VEEAEAEPEEATERTTSIATTTTTTIESVEEVVRVPTTAASITDVA 298
Db 254 VEEAEAEPEEATERTTSIATTTTTTIESVEEVVRVPTTAASITDVA 298

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Db 250 AEEEEPVEEATERTTSIATTTTTTIESVEEVVRVSEQAETGPRAMISRWYDYTF 309
QY 289 -----VPTTAASTPDADV KYLETIPGDENEHAHFQ 317
Db 310 SKCAQFIVGGCGGNRNPNFSDDYCMVAGCGSVTPATAASTPDADV KYLENPNNDENEDRFL 369
QY 318 KAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIOHFQKVESLEQZAAENRQOLVETIHARVEMLNDRRLALENYITALQAVPRPRHIVENMLK 377
Db 370 KAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIOHFQKVESLEQZAAENRQOLVETIHARVEMLNDRRLALENYITALQAVPRPRHIVENMLK 429
QY 378 LVEITHMARVEAMLNDRRLALENYITALQAVPRPRHIVENMLK 437
Db 430 LVEITHMARVEAMLNDRRLALENYITALQAVPRPRHIVENMLK 489
QY 438 EHVVRVDPKAAQIRSOVMTHLRVIERMNSQLLYNYPAVA EIQDEVDLLOKEQNY 497
Db 490 EHVVRVDPKAAQIRSOVMTHLRVIERMNSQLLYNYPAVA EIQDEVDLLOKEQNY 549
QY 498 SDDVLNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL DDLQPHSFSGADSVPA 557
Db 550 SDDVSNMVS DHRVSYGNDAIMPSTETKTVELLPVNGEFSL DDLQPHSFSGADSVPA 609
QY 558 TENVEPVDARPAADRGLTTRPGSGLTNKTETSEIYKVKHDAEF RHDSGYEVHQRKLVFFA 617
Db 610 TENVEPVDARPAADRGLTTRPGSGLTNKTETSEIYKVKHDAEF RHDSGYEVHQRKLVFFA 669
QY 618 EDVGSNKGAIIGLMVGGVVIATVITLVMLKKKQVTSIHGVVEVDAAVTPEERHLSK 677
Db 670 EDVGSNKGAIIGLMVGGVVIATVITLVMLKKKQVTSIHGVVEVDAAVTPEERHLSK 729
QY 678 QQNGYENPTYKFEQMON 695
Db 730 QQNGYENPTYKFEQMON 747

RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - hu
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C:Accession: A32761
R:De Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secr
A:Reference number: A32761; MUID:89346754; PMID:2569763
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain
C:Keywords: cloning artifact

Query Match 57.7%; Score 2105; DB 4; Length 494;
Best Local Similarity 87.7%; Pred. No. 1.4e-103;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;

QY 80 LQIINNVVEANQPTVIONMCKRGKCKTTHPHFVPIYRCVLGVFVS DALLVPDKCKFLHCE 139
Db 1 LQIINNVVEANQPTVIONMCKRGKCKTTHPHFVPIYRCVLGVFVS DALLVPDKCKFLHCE 60
QY 140 RMDVCETHLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDNVDSA 199
Db 61 RMDVCETHLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDNVDSA 120
QY 200 DAEEDSDVMWGADTDYADGSEDKVVEAEVEEAEAEAEAEAEAEAEAEAEAEAEAEAE 259
Db 121 DAEEDSDVMWGADTDYADGSEDKVVEAEVEEAEAEAEAEAEAEAEAEAEAEAEAEAE 180
QY 260 EPEEATERTTSIATTTTTTIESVEEVVRVPTTAASITDVA 288
Db 181 EPEEATERTTSIATTTTTTIESVEEVVRVSEQAETGPRAMISRWYDYTF 240

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QY 289 -----VPTTAASIPDAVDKYLTPGDENEHAFQAKKRL 323
Db 241 FYGGGGRNNFDTREYCMVCGSALPTTAASTPDPAVDKYLTPGDENEHAFQAKKRL 300
QY 324 EAKHRRNSQVREWEAEQAKNLPKADKAVIOHFOEKVSLQEAANEKQQLVETIM 363
Db 301 EAKHRRNSQVREWEAEQAKNLPKADKAVIOHFOEKVSLQEAANEKQQLVETIM 360
QY 384 ARVEAMLNDRRLALENYITALQAVPPRRPHVFNMLKKYVRAQKORQHTLKHFFHVRMY 443
Db 361 ARVEAMLNDRRLALENYITALQAVPPRRPHVFNMLKKYVRAQKORQHTLKHFFHVRMY 420
QY 444 DPKKAAQIRSQVNTHLRVYERMNQSLSLYVPAVAEEIQEV 487
Db 421 DPKKAAQIRSQVNTHLRVYERMNQSLSLYVPAVAEEIQEV 464

RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
K:Alternate names: CDE1-binding protein
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-A-g-1999
C:Accession: A49321; S34644; S40519
R:Spracher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A:Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ex
A:Reference number: A49321; MUID:93250009; PMID:8485127
A:Accession: A49321
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
A:Cross-references: GB:S60099; NID:9300168; PIDN:AAAC60589.1; PID:9300169
A:Experimental source: placenta
A>Note: Sequence extracted from NCHS backbone (NCHS:131198, NCBI:P131198)
R:Von der Kammer, H.; Klaudivy, J.; Hanes, J.; Scheit, K.H.
submitted to The EMBL Data Library, April 1993
A:Description: The human homologue of the murine CDE1-binding protein is an amyloid pre
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <ON>
A:Cross-references: EMBL:222572; NID:9394763; PIDN:CAA80295.1; PID:9394764
R:Waco, W.; Gurbagavatula, S.; Paradis, M.; Romano, D.M.; Siodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A:Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94035131; PMID:8220435
A:Accession: S40519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:9450391; PIDN:AAAC41701.1; PID:9450392
C:Genetics:
A:Gene: GBA:APLP2; APPL2
A:Cross-references: GB:139159; ONIM:104776
A:Map position: 11q23-11q25
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.3%; Score 1728; DB 2; Length 763;
Best Local Similarity 47.1%; Pred. No. 1.7e-83;
Matches 372; Conservative 112; Mismatches 165; Indels 140; Gaps 20;

QY 5 LALLILLAAWTARALEV-----PTDGNAG---LLAEQIAKFCGRLLNMWNGKWDSDP 56
Db 15 LLLLLLVLTALALAGVIEAALNAGTGFAVAEPQIAKFCGRLLNMWNIQTGWEPSP 74
QY 57 SGTKTCIDIKEGILQYQCEVYPELQITNVVNEQPVITQWCKGRKCKCKIHFHFVPIYR 116
Db 75 TGTKSCFEKKEEVLOVQCEVYPELQITNVVNEQPVITQWCKGRKCKCKS--RFVTPFK 132

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QY 117 CLVGEFVSDDLVPDKCKFLHQERQVQVCEETHLHHHTVAKETCSKSTNLHDYGMLLPCGI 176
Db 133 CLVGEFVSDDLVPDKCKFLHQERQVQVCEETHLHHHTVAKETCSKSTNLHDYGMLLPCGI 192
QY 177 DKFRGVEFVCCPLAEESDNVSDADAEEDSDVWVGADTDYADGSDKVVVEAEVEEVAE 236
Db 193 DQFHTETVCCPQTKIGSVSKSEEEDEE-----EEEEEDEEDYDYKSEFFTEAD 245
QY 237 VFE--EEA--DQDDDDDDGDEVEEAEPEY-----EEATERTTSAITTTTITTES 282
Db 246 LEDFTEAAVCDDEDEDEGEVEVEDRDYVYDTFKGDDYNEENPTPGSDGTMSDKETHTD 305
QY 283 VEEV-----VVRP 290
Db 306 VKAVCSQEAHTGPCRAYNPRWYFDLSKQKCVRFYTGCGGGRNNFSEDEDYCMVCKRAMIP 365
QY 291 TTAASITPDAVDKYLTPGDENEHAFQAKKRLQEAANEKQQLVETIM 350
Db 366 PTPLEPND-VDYVYFETSAADNEHAFQAKKRLQEAANEKQQLVETIM 424
QY 351 ADKXAV-QHFOEKVESLEQEAANEKQQLVETIMHARVEAMLNDRRLALENYITALQAVPP 410
Db 425 AERQTEIQHFOAMVKALEKAAASEKQQLVETIMHARVEAMLNDRRLALENYITALQSDPP 484
QY 411 RPRHVENMLKKYVRAEQKORQHTLKHFFHVRMYDPKAAQIRSOVMTHLRVIVERMNQL 470
Db 485 RPRILQALRYVRAEKNDRLHTIRHQVHLAVDPKAAQIRSOVMTHLRVIVERMNQL 544
QY 471 SLLYNVPAVAEEIQEVDELQKQYNSDDVIANISEPRISYGNDAIMPGLTETKTIVE 530
Db 545 SLLYKVPYVAEQIEEDELQKQYNSDDVIANISEPRISYGNDAIMPGLTETKTIVE 587
QY 531 LLPVNGEFSDDLQPMHSGADSVNPANTENVEPVDPARPAADRLITTPGSCLTN----- 585
Db 586 ---VSSSES-EEIPFPHPF--HPFPAJFENB-----DTQPELYHPM--KKGSGVGEQDGG 635
QY 586 IKTEE--ISFVKMDAEFRHDSGYEVHVKLVFAEDVGS-----NKG 625
Db 636 IGAEKVINSKNKYDENMVIDETLDV--KEMTFNARVGVGLEEERESVGPLRDFDSLS 692
QY 626 AITGLMGVGVVIAIVITVVLKXKQYTSIIHGVVEVDAAVTPPEERHLKSMOONGYENP 685
Db 694 ALIGLLVIAVAIATVVISVWLKRGQYTGSHGIVEVDPMITPEERHLKMKMNGHYENP 753
QY 686 TYKFEQMQ 694
Db 754 TYKLEQMQ 762

RESULT 8
S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid p
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type protein

```

C:Keywords: alternative splicing

F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.0%; Score 1716; DB 2; Length 765;
Best Local Similarity 46.2%; Pred. No. 7.2e-83;
Matches 364; Conservative 122; Mismatches 166; Indels 136; Gaps 20;

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QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPOIAMFCGR:NMHMVQNGKWSDP 56
DB 15 LVLLLLGLGTAPAAALAGYIEALANAGTGFVAEPOIAMFCGLNMHVNIQTCKWEPDP 74
QY 57 SGTKICIDITKEGILQYCOEYVPELOITNVZANGPVTIONCKRGKCKOCTHPHFVPIYR 116
DB 75 TGTKSLCTGKEVLYQCOEYVPELOITNVMEANQPNVINDSWCRDRKQCKS--HIVTFPK 132
QY 117 CLVGFEVSDALLVPDKCKFLHQRMDVCETHLHHVTYAKETCSKSTNLDHYGNLLPCGI 176
DB 133 CLVGFEVSDVLLVPDNCQFFHQRMEVCEKHQRHWTLVKEACLTGGLTLYSGMLPCGV 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYA--DGSEDKVYVVAEEER 233
DB 193 DQFHGTGYVCCPQTKVYDSSTMSKEEBEER---DEEDYALDKSEFTPEADJEDFT 248
QY 234 VAEVEEBEADDEDEDDEVEEAEPEYEE-----ATERTISTATTTTTTSEVEVV 287
DB 249 EAAADEDEDEEBEVEEEDRDYDYSFKGDDYNEENPTPESSDGLISDKEIAHDV 308
QY 288 R-----VPT 291
DB 309 KAVCSQEAATGPCRAVMPRWYFDLSKGKCVRFYGGCGGNRNNFESDYCMGVKTIIPR 368
QY 292 TAASPTDAVDKYLETGPDENEHAHFQKAKERLEAKHRRMSQVMPWEAEASQAKNLPKA 351
DB 369 TPLPTND--VDYFETSADNEHARFQKAKEQLEIHRHRMDRVRKKEEAEQLQAKNLPKA 427
QY 352 DKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRJALENYITALQAVPR 411
DB 428 ERQTLIQHFOAMVKALEKAASEKQOLVETHLARVEAMLNDRRRJALENYLAALQSDPR 487
QY 412 PRHVENMLKKYVRAEQKQROHTLKHFEHVRMVDPKAAQIRSQVMTHLKVIERKNQSL 471
DB 488 PHRIQLALRRYVRAENKDRLHTIRHYOHLAVDPDEKAAQMSQVMTHLKVIERKNQSL 547
QY 472 LLYNYPAAVEEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMPSEIKTIVEL 531
DB 548 LLYKYPYVAQEQEIDELQEQR-----ADM-----DQFTSSISSENTPVDR- 589
QY 532 LPVNGEFLDCLQPHWSFGADSPANTENEVEPVDAHFAADRGLTRPGSGITN----- 586
DB 590 --VSSEES--EIPFPHPF--HPFPSENE-----DQPELYHPM--KKGSGMAEQDGLI 638
QY 587 KTEE---ISEVKMAEAFRHDSGYEVHHQKLVFFAEVGS-----NKGA 626
DB 639 GAFEVKNSKNKMDENMVIDETLDV--KEMIFNAERVGGI:KEEIPSVGFLREDFSLSSSA 696
QY 627 IIGLVGVGVVIAIV:VITVLMKKKQYTSIHIGVVEVDAAVTPEERHLSKMGQNGYENPT 686
DB 697 IIGLVVIAVIAIVIVISLVMKKRQYGTISHGIVEVHPMLTPEERHLNKKGNHGYENT 756
QY 687 YKFFEQMQ 694
DB 757 YKYLEQMQ 764
```

RESULT 9

A49974

beta-amyloid precursor protein 2 homolog APLP2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C:Accession: A49974

R:Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.

J. Biol. Chem. 269, 2637-2644, 1994

A:Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid

A:Reference number: A49974; MUID:94132029; PMID:8306594

A:Accession: A49974

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-751 <SU3>

A:Cross-references: GB:C15571; NID:g558467; PIDN:AAA50603.1; PID:g558468

A>Note: sequence extracted from NCBI backbone (NCBI:P:144636)

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote

F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.7%; Score 1704; DB 2; Length 751;

Best Local Similarity 45.9%; Pred. No. 3e-82;

Matches 363; Conservative 113; Mismatches 159; Indels 156; Gaps 20;

```
QY 5 LALLLLAANTARALEV-----PTDGNAG---LIAEPOIAMFCGR:LNHMVQNGKWSDP 56
DB 15 LVLLLLGLGTAPAAALAGYIEALANAGTGFVAEPOIAMFCGLNMHVNIQTCKWEPDP 74
QY 57 SGTKICIDITKEGILQYCOEYVPELOITNVZANGPVTIONCKRGKCKOCTHPHFVPIYR 116
DB 75 TGTKSLCTGKEVLYQCOEYVPELOITNVMEANQPNVINDSWCRDRKQCKS--HIVTFPK 132
QY 117 CLVGFEVSDALLVPDKCKFLHQRMDVCETHLHHVTYAKETCSKSTNLDHYGNLLPCGI 176
DB 133 CLVGFEVSDVLLVPDNCQFFHQRMEVCEKHQRHWTLVKEACLTGGLTLYSGMLPCGV 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAE---E 231
DB 193 DQFHGTGYVCCPQTKVYDSSTMSKEEBEER---DEEDEEDYDLDKSEFFPIE 243
QY 232 BEVAVEEBEAD--DEDEDGDEVEEE-----AEPYEEATERTISTATTI 276
DB 244 ADLEDFTAAADEEBEVEEVEDRDYDYSFKGDDYNEENPTPESEGTIS----- 298
QY 277 TTTTSEVEV----- 286
DB 299 --DKIEVHDVKAVCSQEAATGPCRAVMPRWYFDLSKGKCVRFYGGCGGNRNNFESDYC 356
QY 287 -----VVPVPTAASPTDAVDKYLETGPDENEHAHFQKAKERLEAKHRRMSQVMPWEAE 341
DB 357 MAVCKAMIPPTPIPTND--VDYFETSADNEHARFQKAKEQLEIHRHRMDRVRKKEEAE 415
QY 342 ERQAKNLPKAKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRJALENY 401
DB 416 ELQAKNLPKPTERQTLIQHFOAMVKALEKAASEKQOLVETHLARVEAMLNDRRRJALFN 475
QY 402 ITALQAVPPRRHVENMLKKYVRAEQKQROHTLKHFEHVRMVDPKAAQIRSQVMTHLVR 461
DB 476 LAALQSDPPRPHRIQLALRRYVRAENKDRLHTIRHYOHLAVDPDEKAAQMSQVMTHLHV 535
QY 462 IYHRMNSLSLLYNYPAAVEEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMPSEI 521
DB 536 IERNSQSLSLIKVPYVAQEQEIDELQEQR-----ADM-----DQFTSS 578
QY 522 LTERKTIVEL:LPVNGEFLDCLQPHWSFGADSPANTENEVEPVDAHFAADRGLTRPGSG 581
DB 579 ISENPVDRVSSEES--EIPFPHPF--HPFPSENE-----GSGMAEQDQ- 621
QY 582 GLTNKIKTETI--SEVKMAEAFRHDSGYEVHHQKLVFFAEVGS-----N 623
DB 622 GLIGAEKVKNSKNKMDENMVIDETLDV--KEMIFNAERVGGI:KEEIPSVGFLREDFSL 679
QY 624 KGALIGLVGVGVVIAIV:VITVLMKKKQYTSIHIGVVEVDAAVTPEERHLSKMGQNGYE 683
DB 680 SNALIGLVVIAVIAIVIVISLVMKKRQYGTISHGIVEVDPMLTPEERHLNKKHNGYE 739
QY 684 NPTKYFFEQMQ 694
DB 740 NPTKYLEQMQ 750
```

RESULT 10

A46362

amyloid precursor-like protein; - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:Waco, W.; Bupp, K.; Magendanz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer's disease amyloid beta protein; animal Kuritz-type protease
 A:Reference number: A46362; MUID:93066322; PMID:1279693
 A:Accession: A46362
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCB1 backbone (NCBI:115683; NCBP:118684)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kuritz-type protease
 C:Keywords: transmembrane protein

Query Match 32.5%; Score 1185; DB 2; Length 653;
 Best Local Similarity 38.6%; Pred. No. 4, 9e-55;
 Matches 270; Conservative 121; Mismatches 231; Indels 78; Gaps 17;

QY 1 MPEGLALLLAAMTARA-LEVPDGNAGLLAEPIAMFCGRLLNMNMVONGKWDSDPSGT 59
 DB 22 LPL-LSLILRAQLAVGNLAVGPSAAEAPGSAOVAGLCCRLTLMRLKATGWEPFPQS 80
 QY 60 KTCIDTKEGILQYCOEYVPELQITNVVEANQPVTIQNWCKKGRKCKCTHPHF-VIFYRCL 118
 DB 81 RRLDLPQVLYCYROMYPELHARVEQAQAIPHEWCGGTSGRCALPHVEVYFHLCL 140
 QY 119 VGEFSDALLVPDKKFLHQRMDVGETHLHWHITVAKC:CEKSTNLHDYGMGLPCGDIK 178
 DB 141 PGFVSEALLVPGCRFLHQRMDVCESTRHOEAOACSSGGLILHSGMGLPCGSDR 200
 QY 179 FRGVFVCCPLAESDNVSDADEEDUDVW-WGACIDYACSEPKVVEAFEEVAEV 237
 DB 201 FRGVFVCCP-PPAIPNPSGMAAGDSTKSWPLGGK-AAAAAGGCD-EEVES 248
 QY 238 EEEFAEDDEDEGDEVEEAEPEEATERTIS:ATITTTTESVEEVVRYPT-AASTP 297
 DB 249 PQVDQYFVEPPQAEDEEEERAPPPSPHPVSVRYPTPR-PT-PT-PT-PT-PT-PT-PT-PT 294
 QY 298 DAVDKYLETPGDENEHAFUKAKERLEAKHRMSQVMEHFEAEPAQAKNIPKADKAVI 357
 DB 295 DGVGVYFGMPGETGEHEGF-KAKMDLEERMRMOINEMRENAADSSQKLEKADQALN 354
 QY 358 QHPQEKVESLEOEAANERQOLVETHMARVEAM:NDRERLALENYITALQAVPRPKHVEN 417
 DB 355 EHFQSIQTILEQVSGERQKLVETHATRVIAITINDORRAALGFTAAALQGDPPQAEVLM 414
 QY 418 MLKKYVRAEQQRCHTLKHFHEHYVMVDPKKAQAIRSQVMTHLRV:YERNMQSLGLYNPV 477
 DB 415 ALARYLRAEQEKQHTLRH'QHVAADVPEKAQOMRFQVOTHLQVIERKNGSLGLLDQNP 474
 QY 478 AVAEELODEVELLQKQNY'SDDVLANNMISEPRI:SYGNDAIMP-SUTETKTTVYGLLPVNS 536
 DB 475 HLAQELRPQTELL-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA 510
 QY 537 EFS:DDLOPHSFGADSVANTENEVPVDARAADRGTLTRPGSGLTINIKTEEISEVKM 596
 DB 511 -----GSLQP-----PSKDDPPVTLB-AAA-KGSTDQESSSSGREKITPLEQYQ 551
 QY 597 DAEFRHDSGYEVHH-OK-VFFAEVDGSKNGA:IGLMVGGVVVIAIVITVLM-LKKQ 652
 DB 552 KVNASAPRGFPFHSSDIQRDELAPSGTGVSRREALSGLLINGAGGSLIV:SLLLLRKKP 611
 QY 653 YTSIHGQVEAAVTPPEEHLKSKMQNGYENPTYKFEQ 692
 DB 612 YGT:SHGWEVDPMLTEEQQLRELQGHGYNPTYRLEE 651

RESULT 11
 JCI1404

CDEI-box DNA-binding protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
 C:Accession: JCI1404
 R:Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
 Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
 A:Title: A murine sequence-specific DNA binding protein shows extensive local similarity
 A:Reference number: JCI1404; MUID:93129193; PMID:1482349
 A:Accession: JCI1404
 A:Molecule type: mRNA
 A:Residues: 1-511 <VID>
 C:Comment: This protein plays an important role in the early development of the mouse
 C:Keywords: DNA binding; transmembrane protein

Query Match 31.3%; Score 1143; DB 2; Length 511;
 Best Local Similarity 45.8%; Pred. No. 5, 8e-53;
 Matches 253; Conservative 92; Mismatches 128; Indels 80; Gaps 16;

QY 174 CGIDKFRGVFVCCPLAE--ESDAVDSADAEEDSDVMWGADTDYAPGSEDKVVEVAE- 230
 DB 6 CGVDQFHGTETVCCPQ:KTVDSDSMTSKEEEEE-----DEDEEDYDLKSEF 56
 QY 231 --EEVAVEVEEAD-DEDEDEKIDEVEEAE-----EPYEEATERTIS:ATTTTI 279
 DB 57 PTEALEDFTEAAADEEE:EEEGEEVEVEDRDYVDPFKGDYNE--ENPTSPSEGTIS 314
 QY 280 TESVEEVVRYPTTAAS:PDADVKEYLETPGDENEHAFQKAKERLEAKHRMSQVMEHFE 339
 DB 115 DKEIVHDVKVYPTPLPTND-VDVIFETSADNEHAFQKAKERLEIRNRMRVKKEWE 173
 QY 340 EAERQAKNIPKADKAVI:HQFEKVESLEQEPAAERQOLVETHMARVEAM:NDRERLALE 399
 DB 174 EAE-QAKNLPKTEROTLL:QHPQAMVKALEKAASEKQOLVETHLARVEAM:NDRERLALE 233
 QY 400 NYITALQAVPRPKHFMKAKYVRAEQKDRQHTLKHFEHYVMVDPKKAQAIRSQVMTHL 459
 DB 234 NYLAALSDPPRPHRIQALRRYVRAENKORLHTIRHQVLAVDPEKAAQOMKSOVMTHL 293
 QY 460 RVIVERMNOS:SLIYNVFAVAEEIQDEVELLQKQNY'SDDVLANNMISEPRI:SYGNDAIMP 519
 DB 294 HVIERRNQOS:SLIKVVPVYAEIQEIDELELQOR-----ADM-----DOFT 336
 QY 520 PSLITKTKTIVELLPVNGEFLSDUQPHSFGADSVANTENEVPVDARAADKGLTTRP 579
 DB 337 SSISENPVDVRYSSSESE-EIPPPHPLHPF-----PSLSENE-----GSGMAEQD 380
 QY 580 GSGLTNIKTEEL-SEVKMDAEFRHDSGYEVHHQKLVFEAFDVG- 622
 DB 381 G-GLIGAEKVINSKNMNDENNVIDEIDLDV--KEMIFNAERVGGLEEPESVGPREDPS 437
 QY 623 -NKGAIIGLMVGGVVVIAIVITVLMKKKQYTSIHGQVEVDAAVTPPEERHLKSKMQNG 681
 DB 438 LSSNALIGLLVIAVAIAIVISLVMKRYGIISHGIVEVDPMLTIEERHLKKNMNHG 497
 QY 682 YENPTYKFEQMQ 694
 DB 498 YENPTYKLEQMQ 510

RESULT 12
 JCI5795
 hypothetical protein C42D8.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
 C:Accession: T15795; A49414
 R:Hallsworth, K.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid C42D8.
 A:Reference number: Z18405
 A:Accession: T15795
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-686 <HAL>

A:Cross-references: EMBL:U56966; NID:q1293844; P1D:q123850; P1UN:AA98722.1; GSFEB:GN00
A:Experimental source: strain Br-stcl N2; clone C42D8
R:Daigle, J.; Li, C.
Proc. Natl. Acad. Sci. U.S.A. 95, 12045-12049, 1998
A:Title: ap1-1, a Caenorhabditis elegans gene encoding a protein related to the human beta
A:Reference number: A49414; M3ID:94089766; PMID:5255666
A:Accession: A49414
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 7-686 <DAI>
A:Cross-references: GB:U00240; NID:q416296; P1DN:AAC4670.1; P1D:q416297
C:Genetics:
A:Map position: X
A:Gene: CESP:C42D8.8
A:Introns: 22/3; 78/3; 121/1; 109/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 562/3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 22.4%; Score 817.5; DB 2; Length 686;
Best Local Similarity 29.1%; Pred. No. 1.1e-35;
Matches 222; Conservative 110; Mismatches 275; Indels 155; Gaps 22;

QY 1 MLPGLALLLAATARALETVPDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGIK 60
DB 5 LMIGLLIPILVA-TVYAESPAAGSRHKEKIPWAFSGGYRQYM-TEEGSMKIDDERYA 63

QY 61 TCIDTKEGILQYCEVPELQITNVVEANQPVYTONCKRGKQCKTHPHFVYPCVLVG 120
DB 64 TCFSGKDLKCYRKAYPSMTNITVEYSHEVTSIDMCREEGSPCK-WTHSVRPHYC-DG 122

QY 121 EFSVDALLVPCKFLHQERMDVCEHLRHWHVAKETCEKSTN-----LMDGMLLPG 174
DB 123 EFHSEALQVPHDCQFHSVNSRQCNQNDYGHWDKQCKTKKSGNKDMIVRSFAVLEPC 182

QY 175 GTDKFRGVFEVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDSKYVEAEDEV 234
DB 183 ALDMFTGVFEVCCP-----NDQTNKTDVQTK----- 209

QY 235 AEVEEEADDDDEDGDEVEEAEPEEATER-TSTATTTTTTESVEEVVVPITAA 294
DB 210 ---EDEDDEDDADYEDDYSEEDKDEE----- 236

QY 235 STPDADVKYLETPTGDEHAFQKAKERLEAKHRMSQVKNREBEA-----EROAKNLP 349
DB 237 -EPSSQDFFYKIANWTNEHDFKKAEMRDEKHKKKVDKVNKENGDLTRYNEQKAKD-P 294

QY 350 KADKRAVQ---HFOEKVESLEQFAANERQQLVTHMARVEXAMNDRRRLALENYITAL- 405
DB 295 KGAERFKSQMNARFQKTVSSLPFEHKKRMRKETEAHVHFERVOAKLNEKKREGATHDYRQAZA 354

QY 406 -QAVPPRPHVFNMLKKYVRAECKDRHILKHFHVRMVDPKKAQIISQVMTH-LRVIVE 464
DB 355 THVKNPKNHSVLQSLKATIRAEKDRMHLNRYRHLKADSKAAVYKPTVHRLRYDL 414

QY 405 RMNQSLSLYNVP-----AVA--BEIQEVDELLQKQNYSDCVLANMINSEFRISY 513
DB 415 RINGTLAMLRDPFDLEKYVRPIAVYWKQYRDEVSFD-SVE-----DSELIPIIHODEFSK 470

QY 514 GN--DALMPSLT-----EYKTTVELLPVNGEFS-DELOPKWHSPCADSVANT-----HNEVEP 564
DB 471 NAKLDVKAPTTTAKPVKETDNKAVLPTEASDSEEEACEYDEDEQVKKIPDMKKVKV 530

QY 565 VDARP-----AADRGILTTRPGSLTNIKTEE-----ISEVKDA 598
DB 531 VDIKPKKVTITEBKAKAPKLVTESVQTDDEDDDDSSSTSSSESDSDNNKIKRVDI 590

QY 599 E-----FRHDSGYEVHHQKLVFEAFEDVGSNKGAIIGLMVGQWIAIVILVMLK 649
DB 591 EPIIDEPASFYRD-----KLQSPSEVERSSASVQPVYLASAMPITA-CIIAPAIT 642

QY 650 KQYTSIIHGVVEVDAAVIPEERHLSKMOONGYENPTYKFFE 691
DB 643 NARRRRAMRGFTEVD-VVTPPEERHVAGQVNGYENPTYSFED 683

RESULT 13

A32758
beta-amyloid-like protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 24-Sep-1998
A:Accession: A32758
K:Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989
A:Title: A Drosophila gene encoding a protein resembling the human beta-amyloid p
A:Reference number: A32758; M3ID:89184650; PMID:2494667
A:Cross-references: GB:U04516; NID:q158371; P1D:q158372
C:Genetics:
A:Gene: FlyBase:Appl
A:Cross-references: FlyBase:FBgn0000108
C:Keywords: transmembrane protein

Query Match 20.5%; Score 747; DB 2; Length 886;
Best Local Similarity 25.5%; Pred. No. 7.7e-32;
Matches 233; Conservative 127; Mismatches 288; Indels 264; Gaps 23;

QY 7 LLLAAMTARALEVPTDGNAGLLA-----EPQIAMFC--GRLNMHNV-ONGKWDSPSG 58
DB 9 LLLRSLWVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIYQPYLSEGRWVTDLSK 63

QY 59 T---KTCIDTKEGILQYCEVPELQITNVVEANQPVYTONCKRG---RKQCKTHPHFV 112
DB 64 KTTGPTCLRKMDLLDYCKKAYPNRDTNIVESHYQKIGWCRCQAGLNAAKCKGSHRWI 123

QY 113 IYRCLVGEFVSADALLVPCKFLHQERMDVCEHLRHWHVAKETCEKSTINLHDYQMLL 172
DB 124 KPRFCL-GPFQSDALLVPEGCLFDHIIHNASRCWPFVRWNO-GAAACQERGMQMTFAML 182

QY 173 PCGIDKFRGVFEVCCP-----LAEEEDNDV---SA 199
DB 183 PCGISVFSGVFEVCCPCKEFTDETHVKKTDLPVWFAAQINSADEIMNDEDDSDNSYSK 242

QY 200 DAEEQSDSVWVGADTDYADGSEKVVVEAEFEV-----AEV 237
DB 243 DANEDLLD-----DEDLMGDDDEDDWVADEAATAGSPNTGSSGDSNSGSLDINAEY 296

QY 238 EE-EEADDDDEDGSDRVEEAEVY-----BEATERT 269
DB 297 DSGEGONYEEDGAGSEAEVEASWDSQGAQVSLKSDSSSPSSAPVAPAEKAPVKS 356

QY 270 TSIATTTITTESVEEV-----RVPTTAATPDADVKYLETPTGDEHAFQK 318
DB 357 ESVTSTPQLSASAAAFVAANSNGSGTGAGAPPSTAQPTS---DPYTFHDPHYEQSYKV 413

QY 319 AKERLEAKHRMSQVKNREBEAEERQAKNLPKADKKA-----VIQHFQKVESLEQEA 371
DB 414 SOKRLEESREKVRVMKWDSDLEEKYQDMRLADPKAAQSFQKQMTARFQTSVQALBEEG 473

QY 372 ANERQQLVETHMARVEAMNDRRRLALENYITALQAVPPRPHVFNMLKKYVRAEQDRQ 431
DB 474 NAEKHOLAAMHQORVLAHINQKREAMTCYTOALTQEPNNAHHVEKCLOKLLRALHDKRA 533

QY 432 HTLKHFH-VRMVDP---KKAQIQRQVMTHLRYIYERMNQSLLLYNVPAVEEI---- 483
DB 534 HALAHYRHLNSGGPGGLEAAASERPTLERLIDIDRAVNSQMTMIKARYPELSAKIAQLM 593

QY 484 -----QDEV----- 487
DB 594 NDYILALRSKDDIDPGSSLGNSEAEAGILDKRYVEIERKVAEKERLRLAEKQREAAE 653

QY 488 -----DELLQKEQNYSDVLANMISE-----PRISYGNDAIM 519
DB 654 REKLREKRLREAKVVDMLKSVQAEQSQPTQSSTOSQAOQOQOQEKSLPGKLGPDAAAL 713

QY 520 -----PSLTETKTVYELLVNGEFLSDLOPWHSGFADSVFPAFTENVEPVCAKPRADRG 574
Db 714 VTAANPLETTKS-----EKDLSDTF-----YGEATVSTTKVQTIVLPTVJDDAVQRA 760
QY 575 LTRPGSLINIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FALDVGSKN---GA 626
Db 761 VEDVANA-----VAHGEAPQVQHFTHDLGHRESSFSLRREFAQHAAKGRNV 811
QY 627 IGLMWGGVVIATVITLMLKKQYTSIH-HGVVEVDAVTF-----EERHLSKMQQ 679
Db 812 YFTLSFAGIALMAAFVGVAVAKWRISRSRPAQGFTEVDQNVITHHPVIVREKIVPMQI 871
QY 580 NGYENPTYKFE 691
Db 872 NGYENPTYKFE 883

RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May 1996
C:Accession: S38344
R:Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A:Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A:Reference number: S38344; MUID:94032480; PMID:8218408
A:Accession: S38344
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-246 <HAN>
A:Cross-references: EMBL:222592
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 19.3%; Score 706; DB 2; Length 246;
Best Local Similarity 51.5%; Pred. No. 2.2e-30;
Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;
QY 5 LAULLAANTARALEV-----PTDGNAG---LIAEPTQIMFCGLNKNKNVQKCKDSOP 56
Db 15 LVVLVLGLTAPAAALAGYTEALAAAGTGAFAEPTQIMLCCKLNKNV:QTKRKEPOP 74
QY 57 SGTKICIDTREGILOVCEVVPQLQITNVVEANQPTI:GNMKRGRKCKOCTHEHVIPTPR 116
Db 75 TGTKSCLCITKEVLOVQCEIYPELQITNVMEANQPVNIDSWCRDRKROCKS--HIVIPK 122
QY 117 CLVGFVSDALLVPHKCKFLHQERMDVCEITHLHWHTVAKETSEKSTNLDHYCKMLPCGI 176
Db 133 CLVGEFVSDVLLVPDNCQFFQERMEVCEKHQRWHTLVKEACLTESGLTLYSGKLLPCGV 192
QY 177 DKPRGVEFVCCPLAEESDNDVSADAEEDSDVWGGADTDYADGSEDKVVEAEHFEVAE 236
Db 193 DQFHGTIVCCP---QTKTVDS-----DSIMSKEEEEE--- 222
QY 237 VESEADDED-DEDSGEVEFEAE 259
Db 223 -EEDERDEEDYDLKSEFFTEAD 245

RESULT 15
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Marohn, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: PQ0438; MUID:93075180; PMID:1445331
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide 1
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome
Query Match 11.3%; Score 411; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 581 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATV 640
Db 1 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATV 60
QY 641 IVITLVMKKKKQYTSIHGHVVE 662
Db 61 IVITLVMKKKKQYTSIHGHVVE 82

Search completed: October 2, 2003, 14:00:31
Job time : 20.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 : Search time 16 Seconds

(without alignments)
3277.761 Million cell updates/sec

Title: US-09-806-194-16

Perfect score: 3651

Sequence: 1 MLFGLALLLAANTARALEV.....QQNGYENPTYKFEQMOKK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3590.5	98.3	770	1 A4_HUMAN	P05067 h amyloid b
2	3590.5	98.3	770	1 A4_MACFA	P53601 m amyloid b
3	3584	98.2	751	1 A4_SAISC	O95243 s amyloid b
4	3535.5	96.8	770	1 A4_PIG	P73307 s amyloid b
5	3522.5	96.5	770	1 A4_CAVPO	Q60495 c amyloid b
6	3493.5	95.7	770	1 A4_MOUSE	P12023 m amyloid b
7	3493.5	95.7	770	1 A4_RAT	P08592 i amyloid b
8	1735	47.5	695	1 APP2_MOUSE	Q05335 mus musculu
9	1728	47.3	763	1 APP2_HUMAN	Q05481 homc sapien
10	1716	47.0	765	1 APP2_RAT	P15843 rattus norv
11	1190	32.6	650	1 APPI_HUMAN	P51693 homo sapien
12	1185	32.5	653	1 APPI_MOUSE	Q03157 mus musculu
13	817.5	22.4	686	1 A4_CAEEL	Q10551 caenorhabdi
14	748.5	20.5	887	1 A4_DROME	P14599 drosophila
15	292	8.0	59	1 A4_BOVIN	Q28053 bos taurus
16	288	7.9	58	1 A4_RABIT	Q28748 cryptotagus
17	288	7.9	58	1 A4_SHEEP	Q28757 ovils aries
18	287	7.9	58	1 A4_CANFA	Q28290 canis fami
19	283	7.8	57	1 A4_URSKA	Q29149 ursus marit
20	185.5	5.1	407	1 IE68_HSVSA	Q01042 herpesvirus
21	185.5	5.1	993	1 SGP1_MOUSE	Q62205 mus musculu
22	176	4.8	2034	1 M22_HUMAN	Q92734 homo sapien
23	175.5	4.8	802	1 NAB1_YEAST	P38996 saccharomyc
24	174	4.8	579	1 G150_HUMAN	Q08378 homo sapien
25	173.5	4.8	793	1 CALD_HUMAN	Q05682 homo sapien
26	172	4.7	771	1 CALD_CHICK	P12957 gallus gall
27	169.5	4.6	297	1 TRT2_HUMAN	P45379 homo sapien
28	169.5	4.6	721	1 YCF2_OENPI	P31568 oenothera p
29	168.5	4.6	1875	1 MDP1_YEAST	Q02455 saccharomyc
30	168	4.6	1240	1 YNUL_YEAST	P35935 saccharomyc
31	167.5	4.6	1976	1 MYHA_HUMAN	P35580 homo sapien
32	166.5	4.6	816	1 YG3A_YEAST	P53276 saccharomyc
33	166.5	4.6	1976	1 MYHA_RAT	Q93100 rattus norv

34	164.5	4.5	1325	1 G160_MOUSE	P55937 mus musculu
35	163.5	4.5	681	1 MP10_HUMAN	O00566 homo sapien
36	163	4.5	2017	1 MYSN_DROME	Q99323 drosophila
37	162.5	4.5	712	1 NUCLE_RAT	P13383 rattus norv
38	160.5	4.4	1976	1 MYHA_BOVIN	Q27991 bos taurus
39	160	4.4	694	1 NUCLE_CHICK	P15771 gallus gall
40	159.5	4.4	1955	1 PJMA_PARUN	O61308 parascaris
41	158	4.3	301	1 TRT2_CHICK	P02642 gallus gall
42	157.5	4.3	706	1 NUCLE_HUMAN	P19338 homo sapien
43	156.5	4.3	1332	1 SPT1_YEAST	P35177 saccharomyc
44	156.5	4.3	5596	1 MDN1_HUMAN	Q9nu22 homo sapien
45	156	4.3	1433	1 REST_CHICK	O42184 gallus gall

ALIGNMENTS

RESULT 1
A4_HUMAN STANDARD; PRT: 770 AA.
ID AC P05067; P09000; P78438; Q13778; Q13793; Q16011; Q9BF38;
AC Q9UCB6; Q9U058;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[.]
SEQUENCE FROM N.A. (ISOFORM APP695).
TI SSUP-Brain;
EX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
cell-surface receptor.";
RL Nature 325:733-736(1987).
[2]
SEQUENCE FROM N.A. (ISOFORM APP751).
TI SSUP-Brain;
RC MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
protease inhibitors.";
RL Nature 331:525-527(1988).
[3]
SEQUENCE FROM N.A. (ISOFORM APP695).
EX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
[4]
SEQUENCE FROM N.A. (ISOFORM APP770).
EX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
gene.";

RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RX Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.:
 RL Gene 102:291-292(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92286136; PubMed=1587857;
 RA Koenig G., Moening U., Czern C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.:
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells."
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9103164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.:
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus."
 RL Nucleic Acids Res. 25:1302-1308(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grosse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Auetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Parker A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson P.D., McElhinny S.C.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hite S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.S.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield A.S., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.:
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.:
 RT "A cDNA specifying the human amyloid beta precursor protein (AβPP)
 RT encodes a 95-kDa polypeptide."
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [10]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.:
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [11]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Ferla G., Lahiri D.K., Satton S.R., Robakis N.K.:
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene."
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [12]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.:
 RT "Purification of protease nexin II from human fibroblasts."
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.:
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein."
 RL Science 245:651-653(1989).
 RN [14]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ranakrishna N., Wolfe G., Wisniewski H.M.:
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [15]
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Nere R.L.:
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease."
 RL Nature 331:528-530(1988).
 RN [16]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.:
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity."
 RL Nature 331:530-532(1988).
 RN [17]
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Choo W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.:
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [18]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.:
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I."
 RL J. Biol. Chem. 271:1614-1620(1996).
 RN [19]
 RP SEQUENCE OF 656-737 FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.:
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor."
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [20]
 RP SEQUENCE OF 672-681.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88035004; PubMed=3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.:
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels."
 RL J. Neurochem. 49:1394-1401(1987).
 RN [21]
 RP SEQUENCE OF 674-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87120328; PubMed=3810169;
 RA Goldberg D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.:
 RT "Characterization and chromosomal localization of a cDNA encoding
 RT brain amyloid of Alzheimer's disease."

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Query Match 98.3% Score 3590.5 DB 1: Length 770;
Best Local Similarity 90.1% Pred. No. 3 2e-17;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEFGIAMEFGRINMHNVNQNKWSDPSGTR 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEFGIAMEFGRINMHNVNQNKWSDPSGTR 60
QY 61 TCIDITKEGILCYGVEYPELQITNVFEANQPVTCNNCKRGKCKOCHPHEVPIYRGLVG 120
DB 61 TCIDITKEGILCYGVEYPELQITNVFEANQPVTCNNCKRGKCKOCHPHEVPIYRGLVG 120
QY 121 EFVSDALLVPCKFLHQRWDVCEHLHWHIVAKETCSEKSTNLHDYGMLLPGGLDKFR 180
DB 121 EFVSDALLVPCKFLHQRWDVCEHLHWHIVAKETCSEKSTNLHDYGMLLPGGLDKFR 180
QY 181 GVEFVCCPLAESNDVSDAEEEDSDVWVGAGTDVADGSECKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESNDVSDAEEEDSDVWVGAGTDVADGSECKVVEAEVEEVEE 240
QY 241 EADDDEDDGDEVEEAEPEYERATERITTSIAITTTTTSVEEVEEVR----- 288
DB 241 EADDDEDDGDEVEEAEPEYERATERITTSIAITTTTTSVEEVEEVR----- 288
QY 289 ----- 288
DB 289 ----- 288
QY 301 RAMISRWFVDTGKCAFFYGGGGGNNRNFDTSPYCMVCGSAMSGELLITDPEIARD 360
DB 301 RAMISRWFVDTGKCAFFYGGGGGNNRNFDTSPYCMVCGSAMSGELLITDPEIARD 360
QY 289 ---VPTTAASPDAVDKYLETPGDENEHAFQKAKERLEAKHREKMSQVMEWEAEARQA 345
DB 361 PVKLPTTAASPDAVDKYLETPGDENEHAFQKAKERLEAKHREKMSQVMEWEAEARQA 420
QY 346 KNLPKADKAVIQHFOEKVESLEQEAANEERQQLVETHMARVEMLNDRRRLALENYTAL 405
DB 421 KNLPKADKAVIQHFOEKVESLEQEAANEERQQLVETHMARVEMLNDRRRLALENYTAL 480
QY 406 QAVPPRPRHVNMLKKYVRAEKQDRHTLKHFHVRVMDPKKAAQIRSOVATHLRVIVYER 465
DB 481 QAVPPRPRHVNMLKKYVRAEKQDRHTLKHFHVRVMDPKKAAQIRSOVATHLRVIVYER 540
QY 466 MNQSLSLYNNPVAEEIODEVELLQEQNSDDVLANMISEPISYGNDAIMPSTET 525
DB 541 MNQSLSLYNNPVAEEIODEVELLQEQNSDDVLANMISEPISYGNDAIMPSTET 600
QY 526 KTIIVELLVNGEESLDLQPHRSFGADSVPAANTEVEFVAPARPAADRGILTTPGSGGJTN 585
DB 601 KTIIVELLVNGEESLDLQPHRSFGADSVPAANTEVEFVAPARPAADRGILTTPGSGGJTN 660
QY 586 IKTEISIFVKMDAEPHSDSGYEVHHQKLVFFAELVGSNKGAIIGLVGSGVVIATVIVITL 645
DB 661 IKTEISIFVKMDAEPHSDSGYEVHHQKLVFFAELVGSNKGAIIGLVGSGVVIATVIVITL 720
QY 646 VMLKKQYTSIHGVEVDAAVTPERHLSKMQONGYENPTYKTFEQMN 695
DB 721 VMLKKQYTSIHGVEVDAAVTPERHLSKMQONGYENPTYKTFEQMN 770

RESULT 2
A4_MACFA
ID A4_MACFA STANDARD: PRT: 770 AA.
AC P53601; Q95KN7;
DI 01-OCT-1996 (Rel. 34, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(43);
DE Gamma-Ctf(59) (Gamma-secretase C-terminal fragment 59); Gamma-Ctf(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-Ctf(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.
```

```
US Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecinae; Macaca.
CN NCBI_TaxID=9541;
CN [1];
CN SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
CN TISSUE=Cerebellum;
CN MEDLINE=91273117; PubMed=1905108;
CN Podlisky M.B., Tolan D.R., Selkoe D.J.;
CN RA Homology of the amyloid beta protein precursor in monkey and human
CN RT supports a primate model for beta amyloidosis in Alzheimer's
CN AT disease";
CN Am. J. Pathol. 138:1423-1435(1991).
CN -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metallated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein Bdp, FPR1, APPBP1, IBL, KNS2
CC (via its IPR domains) (By similarity). APPBP2 (via BASS) and DBP1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoId=P53601-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PTB domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
```

interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (by similarity).

-1- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (by similarity).

-1- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (by similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (by similarity).

-1- PTM: N- and O-linked glycosylated (by similarity).

-1- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (by similarity).

-1- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (by similarity).

Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (by similarity).

-1- SIMILARITY: BELONGS TO THE APP FAMILY.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL: M58727; AAA36829.1; -
 EMBL: M58726; AAA36828.1; -
 HSP: P05067; IAAP.
 InterPro: IPR001868; A4_APP.
 InterPro: IPR002223; Kunitz_RPT.
 Pfam: PF02177; A4_EXTRA; 1.
 Pfam: PF03494; Beta_APP; 1.
 Pfam: PF00014; Kunitz_BPTI; 1.
 PRINTS: PR00759; BASICPTASE.
 ProDom: PD000222; Kunitz_RPT1; 1.
 SMART: SM00006; A4_EXTRA; 1.
 SMART: SM00131; KU; 1.
 PROSITE: PS00319; A4_EXTRA; 1.
 PROSITE: PS00320; A4_INTRA; 1.
 PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 K W Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 K W Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 K W Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 K W Proteoglycan; Alternative splicing; Amyloid.
 SIGNAL 1 17
 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 688 713 C83 (POTENTIAL).
 FT CHAIN 688 713 P3(42) (POTENTIAL).
 FT CHAIN 688 711 P3(40) (POTENTIAL).
 FT CHAIN 688 711

FT CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FT CHAIN	714	770	GAMMA-CTF(57) (POTENTIAL).
FT CHAIN	721	770	GAMMA-CTF(50) (POTENTIAL).
FT CHAIN	740	770	C31 (POTENTIAL).
FT DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	700	723	POTENTIAL.
FT DOMAIN	724	770	CYTOSOLASMIC (POTENTIAL).
FT DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT DOMAIN	231	341	BPTI/KUNITZ INHIBITOR.
FT DOMAIN	331	423	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT DOMAIN	274	280	POLY-THR.
FT SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT AC1_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT SITE	671	672	CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
FT SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
FT SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
FT SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FT SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FT SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FT SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FT SITE	724	734	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT SITE	739	740	CLEAVAGE (BY CASPASES-3, -6, -8 OR -9) (BY SIMILARITY).
FT SITE	757	760	ENDOCYTOSIS SIGNAL.
FT SITE	759	762	NPXY MOTIF.

Query Match: 98.3%; Score 3590.5; DB 1; Length 770;
 Best local Similarity 90.1%; Pred. No. 3.2e-17;
 Matches 594; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

Qy	1	MLPGIALLLLAAWTAARALEVPTDGNAGLLAPGIAFCGRNLNMHNVONGKWDSPGSK 60
Db	1	MLPGIALLLLAAWTAARALEVPTDGNAGLLAPGIAFCGRNLNMHNVONGKWDSPGSK 60
Qy	61	TCIDTKEGILOVCQEVYPELOITINNVFEANQPTVIONWCKRGKCKCTHPHEVPIYRCILVG 120
Db	61	TCIDTKEGILOVCQEVYPELOITINNVFEANQPTVIONWCKRGKCKCTHPHEVPIYRCILVG 120
Qy	121	EFVSDALLVPKCKFLHQRMDVCHLHWHTVAKETCEKSTNKLHDYGMLLPGIDKFR 180
Db	121	EFVSDALLVPKCKFLHQRMDVCHLHWHTVAKETCEKSTNKLHDYGMLLPGIDKFR 180
Qy	181	GVEFVCCPLAESDNVDSADAFEDSDVWVGADTDYADGSEDKVVEVAEEVAEVEE 240
Db	181	GVEFVCCPLAESDNVDSADAFEDSDVWVGADTDYADGSEDKVVEVAEEVAEVEE 240
Qy	241	EADDDDEDDGDEVEEAEEPEEATERTTSIATTTTTTTSVEVEVVR----- 288
Db	241	EADDDDEDDGDEVEEAEEPEEATERTTSIATTTTTTTSVEVEVVR----- 288
Qy	289	----- 288
Db	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNFTDEEYCMVCGSVMSQSLRKTTRPLTRD 360
Qy	289	---VPTTAASPTDAVDKYLETFGDENEHAHQKAKERLEAKHREHMSQVMREWEAEERQA 345
Db	361	PVKLPTTAASPTDAVDKYLETFGDENEHAHQKAKERLEAKHREHMSQVMREWEAEERQA 420

15-SEP-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CRF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CRF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Kimura A., Takahashi T.;

RT "Amyloid precursor protein 70.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-136 FROM N.A.

RC TISSUE=Small intestine;

RA Winteroe A.K., Fredholm M.;

RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 667-723 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB/rip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity).

CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).

CC -!- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
CC peptides, including C3-, are potent enhancers of neuronal
CC apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK6IP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, EPRL1, APPBP1, IBI, KKS2
CC (via its TPR domains) (By similarity). APPBP2 (via Bass) and APPBP1
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and

CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).

CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).

CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).

CC -!- PTM: N- and O-linked glycosylated (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).

CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----

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CC -----

DR EMBL: AB032550; BA84580.1; -
DR EMBL: Z84022; CAB06313.1; -
DR EMBL: X56127; CAA39592.1; -
DR HSSP: P05067; IAAP.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4-extra.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE; PS00260; BPTI_KUNITZ_1; 1;
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1;
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN;
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 C83 (BY SIMILARITY).
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59).
 FT CHAIN 714 770 GAMMA-CTF(57).
 FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).
 FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 135 155 COPPER-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 667 668 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
 Query Match 96.8%; Score 3535.5; DR 1; Length 770;
 Best Local Similarity 88.4%; Pred. No. 1.7e-168;
 Matches 681; Conservative 8; Mismatches 5; Indels 75; Gaps 1;
 QY 1 MLPGLALLLAATARALETVDGNGAGLAPQAFMFCGRLLNMHMYQNGKWSQPSGCK 60
 Db 1 MLPGLALVLAATARALETVDGNGAGLAPQAVAMFCGRLLNMHMYQNGKWSQPSGCK 60
 QY 61 TCIDTKGILQYCOEYVPELOITNNVEANQPVTTQNMCKRGRKCKTHPHFVPIRCLVG 120
 Db 61 TCIDTKGILQYCOEYVPELOITNNVEANQPVTTQNMCKRGRKCKTHPHFVPIRCLVG 120
 QY 121 EFVSDALLVPDKKFLHQRMDVCETHLHWTVAKETCSKSTNLHDYGMILPGIDKFR 180
 Db 121 EFVSDALLVPDKKFLHQRMDVCETHLHWTVAKETCSKSTNLHDYGMILPGIDKFR 180
 QY 181 GVEFVCCPLAESQNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 Db 181 GVEFVCCPLAESQNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 QY 241 EADDEDEDEGDEVEEAEPEYEAETRTTSIATTTTTTTSVEEVEVVCSEQAEGHC 300
 Db 241 EADDEDEDEGDEVEEAEPEYEAETRTTSIATTTTTTTSVEEVEVVCSEQAEGHC 300

Db 241 EADDEDEDEGDEVEEAEPEYEAETRTTSIATTTTTTTSVEEVEVVCSEQAEGHC 300
 QY 289 -----
 Db 301 RAMISRWYELDTGKCAPFEYGGCGGNRNFPDTEECMAVCGSVMSQSLKTTQEHLPQ 360
 QY 289 ---VPIAASTPDVDKY-ETPGDENEHAHFQKAKERLEAKHRRMSQVMREKEAEQCA 345
 Db 361 PVKLPITAASTPDVDKYLETGPDENEHAHFQKAKERLEAKHRRMSQVMREKEAEQCA 420
 QY 346 KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 405
 Db 421 KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
 QY 406 QAVPPRRHVFNMLKYYVRAEQDKROHTLKHFHVHVMYDPKKAQTRSOVMTHLRVYER 465
 Db 481 QAVPPRRHVFNMLKYYVRAEQDKROHTLKHFHVHVMYDPKKAQTRSOVMTHLRVYER 540
 QY 466 MQOSLLYNPAVAEEIODEVELLOKEQNTSDOVLANMISEPRISYNDALMPSLTET 525
 Db 541 MQOSLLYNPAVAEEIODEVELLOKEQNTSDOVLANMISEPRISYNDALMPSLTET 600
 QY 526 KTTVELLPVNGEFSLDLQPHSHFGADSVDPANTENEVEPVDARPAADRGILTTPGSGLTN 585
 Db 601 KTTVELLPVNGEFSLDLQPHSHFGADSVDPANTENEVEPVDARPAADRGILTTPGSGLTN 660
 QY 586 IKTEELSEYVKMDAEFRHDSGYEVHOKLVFPADVCSNKGATIGLMVGGVVIATVITL 645
 Db 661 IKTEELSEYVKMDAEFRHDSGYEVHOKLVFPADVCSNKGATIGLMVGGVVIATVITL 720
 QY 646 VMLKKQYTSIIHGVEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMON 695
 Db 721 VMLKKQYTSIIHGVEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMON 770
 RESULT 5
 A4_CAVPO STANDARD; PRI: 770 AA.
 ID A4_CAVPO Q60495; Q60495;
 AC Q60495; Q60495;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC "SSUE-Brain, and Liver;
 RX MEDLINE-97236426; PubMed-9116031;
 RA Beck M., Muelier D., Bigl V.;
 RI "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RI alternative splicing.";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE-98007700; PubMed-9349544;
 RA Martel C.L., Meckie J.B., Matsubara E., Governale S., Miguel C.,
 RA Miao W., Mccomb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RI "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RI cerebral capillary sequestration and blood-brain barrier transport of
 RI circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE-20084499; PubMed-10619481;

RA Beck M., Brückner M.K., Holzer M., Kaep S., Kanneke T., Arendt I.,
RA Bigl V.;
RI *Guinea-pig primary cell cultures provide a model to study expression
RI and amyloidogenic processing of endogenous amyloid precursor
RI protein.*;
RI Neuroscience 95:243-254(2000).
RN [4].
RP GAMMA-SECRETASE PROCESSING.
RX MEDLINE-20576391; PubMed-11035007;
RA Pinnix I., Mushnuru U., Fun H., Sridharan A., Goide T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.;
RI "A novel gamma-secretase assay based on detection of the putative
RI C-terminal fragment-gamma of amyloid beta protein precursor.";
RI J. Biol. Chem. 276:481-487(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(s) and G(i) (By
CC similarity). Inhibits G(s) alpha Arpase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen 2 and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC and apolipoproteins E and J in the CSF and to HDL particles in
CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC -!- FUNCTION: Apicicans elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain (By similarity).
CC -!- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APB8 family members, the AFB4
CC family, MAP6IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IB1, KNS2
CC (via its IPR domains), APPBP2 (via BASS) and DBL1 (By similarity).
CC Associates with microtubules in the presence of ATP and in a
CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC ApoE3 appears to be the preferred amyloid binding isoform, while
CC the ApoE4 isoform-beta-Ap40 complex is capable of being
CC transported across the blood-brain barrier.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated pits
CC (By similarity). During maturation, the immature APP (N-
CC glycosylated in the endoplasmic reticulum) moves to the Golgi
CC complex where complete maturation occurs (O-glycosylated and
CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC APP is released into the extracellular space and the C-terminal is
CC internalized to endosomes and lysosomes (By similarity). Some APP
CC accumulates in secretory transport vesicles leaving the late Golgi
CC compartment and returns to the cell surface (By similarity). APP
CC sorts to the basolateral surface in epithelial cells (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms, missing exons 7, 8 and 15, seem to
CC exist. The L-isoforms, missing exon 15, are referred to as
CC apicicans;
CC Name=APP770;

CC IsoId=060495-1; Sequence-Displayed;
CC Name=APP695;
CC IsoId=060495-2; Sequence-VSP_007221, VSP_007222;
CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC brain. The longer isoforms containing the BPTI domain are
CC predominantly expressed in peripheral organs such as muscle and
CC liver.
CC -!- INDUCTION: Increased levels during neuronal differentiation.
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells.
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue (By similarity). The NPXY site is also involved in
CC clathrin-mediated endocytosis.
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments.
CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC gamma-secretase yields p3 peptides. This is the major secretory
CC pathway and is nonamyloidogenic. Alternatively,
CC presenilin/alpha-secretase-mediated gamma-secretase processing of CTF-
CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC and amyloid-beta 42 (Abeta42), major components of amyloid
CC plaques, and the corresponding cytotoxic C-terminal fragments
CC (CTFs).
CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC apoptosis (By similarity).
CC -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC sulfate to the L-APP isoforms produces the APP proteoglycan core
CC proteins, the apicicans (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific (By similarity).
CC Phosphorylation can affect APP processing, neuronal
CC differentiation and interaction with other proteins.
CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X97631; CAA66230.1; -;
CC EMBL: X99198; CAA67589.1; -;
CC HSSP: P05067; IBA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR008154; A4_extra.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF00014; Kunitz_BPTI; 1.
CC PRINTS: PR00203; AMYLOIDA4.
CC ProDom: PD000222; Kunitz_BPTI; 1.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00131; KU; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., McIlahy S.J.,
RA Hosak S.A., McEwen P.J., McKernan K.J., Malok J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Li X., Gibbs R.A.,
RA Fahy J., Helton E., Kettunen M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rouffard G.G.,
RA Blakesley K.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S.N., Krzywinski M.L., Skalska G., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.K., Marisa M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 281-330 FROM N.A., AND ALTERNATIVE SPLICING.
RC --SUG2-Brain, and Kidney;
RX MEDLINE=89149813; PubMed=24933250;
RA Yamada T., Sasaki H., Dohura K., Goto T., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor";
RT Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN [8]
RP SEQUENCE OF 285-364 FROM N.A.
RC STRAIN=CD-1; Tissue=Placenta;
RX MEDLINE=89345111; PubMed=2559710;
RA Fukuchi K., Martin G.M., Deab S.S.;
RT "Sequence of the protease inhibitor domain of the A1 amyloid protein
RT precursor of *Mus domesticus*.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [9]
RP SEQUENCE OF 656-737 FROM N.A.
RC STRAIN=129/Sv;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecechi M.,
RA Loring J.F., Goate A.M.;
RT "Introduction of six mutations into the mouse genome using 'Hit and
RT Run' gene-targeting: introduction of familial Alzheimer's disease
RT mutations into the mouse amyloid precursor protein gene and
RT humanization of the A-beta fragment";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [10]
RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX PubMed=8510506;
RA Sola C., Mengod G., Ghetti B., Palacios J.M., Iriarhou L.C.;
RT "Regional distribution of the alternatively spliced isoforms of beta
RT APP RNA transcript in the brain of normal, heterozygous and
RT homozygous weaver mutant mice as revealed by in situ hybridization
RT histochemistry.";
RL Brain Res. Mol. Brain Res. 17:340-346(1993).
RN [11]
RP INTERACTION WITH KNS2.
RX PubMed=11144355;
RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-1";
RL Neuron 28:449-459(2000).
RN [12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-725;
RP THR-743; TYR-757; ASN-759 AND TYR-762.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niihara T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK";
RL J. Neurosci. 21:6597-6607(2001).
RN [13]
RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX MEDLINE=22628091; PubMed=11312189;
RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki I.;
RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT with scaffold proteins of the JNK signaling cascade.";
RL J. Biol. Chem. 277:20070-20078(2002).

RN [14]
RP INTERACTION OF CTF PEPTIDES WITH NUMB.
RX PubMed=12011456;
RA Roncarati R., Sestau N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA Meucci O., McGlade J.C., Rakic P., D'Adamo L.;
RT "The gamma-secretase generated intracellular domain of beta-amyloid
RT precursor protein binds Numb and inhibits Notch signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN [15]
RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APPB1.
RX PubMed=11553691;
RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT gamma-secretase is rapidly degraded but distributes partially in a
RL nuclear fraction of neurons in culture.";
RL J. Neurochem. 78:1168-1178(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions. Can promote transcription activation through binding
CC to APPB1/Tip60 and inhibit Notch signaling through interaction
CC with Numb. Couples to apoptosis-inducing pathways such as those
CC mediated by G(O) and JIP. Inhibits G(O) alpha Arpase activity (By
CC similarity). Acts as a kinesin I membrane receptor, mediating the
CC axonal transport of beta-secretase and presenilin 1. May be
CC involved in copper homeostasis/oxidative stress through copper ion
CC reduction. Can regulate neurite outgrowth through binding to
CC components of the extracellular matrix such as heparin and
CC collagen I and IV (By similarity). The splice isoforms that
CC contain the BPT1 domain possess protease inhibitor activity (By
CC similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis.
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB family members, the APPA
CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC its serine phosphorylation. Also interacts with GPCR-like protein
CC BPT, FPR1, APPBP1, IBI, KNS2 (via its IPR domains), APPBP2 (via
CC Bass) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC MT-binding domains (By similarity). Associates with microtubules
CC in the presence of ATP and in a kinesin-dependent manner (By
CC similarity). Interacts, through a C-terminal domain, with GNAO1
CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC
CC Query Match 95.7%; Score 3493.5; DB 1; Length 770;
CC Best Local Similarity 87.8%; Pred. No. 2.1e-166;
CC Matches 676; Conservative 6; Mismatches 13; Indels 75; Gaps 1;
QY 1 M L P G A L L L L A A W T A R A L E V P T D G N A G L I A P Q I A M F C G R L N M H M N Y N G K W S D P S G T K 60
DB 1 M L P S L A L L L A A W T R A L E V P T D G N A G L I A P Q I A M F C G L N M H M N Y N G K W S D P S G T K 60
QY 61 T C I D T K E G I Q Y C Q E V Y P E L O I T W V E A N Q P V T T O N M K K R G K O C K T H P F I V I P R C L V G 120
DB 61 T C I G T K E G I Q Y C Q E V Y P E L O I T W V E A N Q P V T T O N M K K R G K O C K T H T H I V I P R C L V G 120
QY 121 E F V S D A L L V P D K C K F L Q E R M D V C E T H L H W H I V A K E T C S E K S T N L H D Y G M L L P G I D K F R 180

RA Liu S.T., Howlett G., Barrow C.J.,
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 of the A beta peptide of Alzheimer's disease.";
 RL Biochem. Biophys. Acta 1586:190-198(2001).
 RN [121]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 GLY-704.
 RX PubMed-11959460;
 RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX PubMed-9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Candy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]
 RP PHOSPHORYLATION ON SER-730.
 RX PubMed-10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 THR-743.
 RX MEDLINE-99274744; PubMed-10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX PubMed-10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX PubMed-11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 contains chondroitin sulfate E in the repeating disaccharide region
 and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in
 cell mobility and transcription regulation through protein-protein
 interactions (By similarity). Can promote transcription activation
 through binding to APBB1/Tip60 and inhibit Notch signaling through
 interaction with Numb (By similarity). Couples to apoptosis-
 inducing pathways such as those mediated by G(O) and JIP. Inhibits
 G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 mediating the axonal transport of beta-secretase and presenilin 1
 (By similarity). May be involved in copper homeostasis/oxidative
 stress through copper ion reduction. Can regulate neurite
 outgrowth through binding to components of the extracellular
 matrix such as heparin and collagen I and IV (By similarity). The
 splice isoforms that contain the BPTI domain possess protease
 inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and tau
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
 CC peptides, including Cβ1, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAP4B1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FRL1, APPB1, IBI, KNS2
 CC (via its TPR domains), APPB2 (via BASS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC pits. Query Match 95.7%; Score 3493.5; DB 1; Length 770;
 Best Local Similarity 87.7%; Pred. No. 2.le-166;
 Matches 675; Conservative 8; Mismatches 12; Indels 75; Gaps 1;
 QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVONGKWDSPGSK 60
 DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVONGKWDSPGSK 60
 QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKCKKTHPHFVPIYRCLVG 120
 DB 61 TCIGTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKCKKTHPHFVPIYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHVAKETCSEKSTNLHVDYGLMLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHVAKETCSEKSTNLHVDYGLMLPGIDKFR 180
 QY 181 GVEFVCCPLAESONVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEVEE 240
 DB 181 GVEFVCCPLAESONVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEVEE 240
 QY 241 EADDEDEDEGDEVEEEAEPEEATERTTSIATITTTTSTESVEEVR----- 288
 DB 241 EADEDEDEGDEVEEEAEPEEATERTTSIATITTTTSTESVEEVR----- 288
 QY 289 ----- 289
 DB 301 RAMISRWFVDTEGKCAPFFYGGCGGNRRNFDEEYCMAGCVSSQSLLKTTSEPLQD 360
 QY 289 ---VFITTAASPDVADKYLETGPDENEHAHQKAKERLEAKHRERMSVOMREWEAEERQA 345
 DB 361 PVKLPITTAAS:PDVADKYLETGPDENEHAHQKAKERLEAKHRERMSVOMREWEAEERQA 420
 QY 346 KNLPRADKAVIQIHFQEKVESLEQEAANEERQOLVETHMARVEAMLNRRRLALENY:ITAL 405
 DB 421 KNLPRADKAVIQIHFQEKVESLEQEAANEERQOLVETHMARVEAMLNRRRLALENY:ITAL 480
 QY 406 QAVPPRPHVFNMLKKYVRACOKORQHTLKHFEHVRVMDPKKAAQIRSQVTHLRVIYER 465
 DB 481 QAVPPRPHVFNMLKKYVRACOKORQHTLKHFEHVRVMDPKKAAQIRSQVTHLRVIYER 540
 QY 466 MNQSLSLNYPVAEEIQDEVDLLOKEQYSDVLANMISEPRISYCNALPSTLET 525
 DB 541 MNQSLSLNYPVAEEIQDEVDLLOKEQYSDVLANMISEPRISYCNALPSTLET 600
 QY 526 KTTVELLPVNGEFSLDDLPNRSFCADSVPAANTEVEPEVDARPAADRGLTTRPGSLTN 585

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Db 601 KITVELLVNGEESDDQPMHPEGVDSVPANTENEVEPVDARPAADKGLTIRGSGLIN 660
QY 586 IKTEISEVKMDAERHDSGVEVHHOKLVFFARVDGSKGAIIGLMVGGVYATVIVITL 645
Db 661 IKTEISEVKMDAERHDSGVEVHHOKLVFFARVDGSKGAIIGLMVGGVYATVIVITL 720
QY 646 VMLKKKQYTSIHGGVVEVJAAVTPERHLSKMQNGVNPYKFFEQMON 695
Db 721 VMLKKKQYTSIHGGVVEVJAAVTPERHLSKMQNGVNPYKFFEQMON 770

RESULT 8
APP2_MOUSE STANDARD: PRT: 695 AA.
AC Q06335;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amyloid-like protein 2 precursor (CDEI-box binding protein.) (CDSBP).
GN APLP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RA von der Kammer H.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-246 FROM N.A.
RX MEDLINE=94032480; PubMed=8218408;
RA Hanes J., von der Kammer H., Kristjansson G.L., Scheit K.;
RT "The complete cDNA coding sequence for the mouse CDEI box-binding
RT protein."
RL Biochim. Biophys. Acta 1216:154-156(1993).
RN [3]
RP SEQUENCE OF 185-695 FROM N.A.
RX SURAIN=BAH/C; TISSUE=Heart;
RL MEDLINE=93129193; PubMed=1462345;
RA Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
RT "A murine sequence-specific DNA binding protein shows extensive local
RT similarities to the amyloid precursor protein."
RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN [4]
RP SEQUENCE OF 1-35 FROM N.A.
RX STRAIN=129/Sv;
RL MEDLINE=96029629; PubMed=7592716;
RA von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT "The mouse APLP2 gene. Chromosomal localization and promoter
RT characterization."
RL J. Biol. Chem. 270:26475-26480(1995).
CC -1- FUNCTION: BINDS TO THE DNA 5'-GTGACATG-3' (CDEI BOX) WHICH PLAYS
CC AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 222592; CAAB0306.1; -
DR EMBL; M97216; AAA20039.1; -
DR EMBL; U34291; AAC52318.1; -
DR PIR; S38344; S38344.
DR HSP; P05067; 1MWP.

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MCD; MGI:88047; Apll2.
DR InterPro: IP001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYL0IDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Transmembrane; DNA-binding; Signal; Nuclear protein.
FT SIGNAL 1..29
FT CHAIN 30..695
FT DOMAIN 30..624
FT TRANSMEM 625..648
FT TRANSMEM 649..695
FT DOMAIN 218..294
FT DOMAIN 218..231
FT DOMAIN 231..266
FT CARBOHYD 485..485
FT CONFLICT 185..189
SQ SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;

Query Match 47.5%; Score 1735; DB 1; Length 595;
Best Local Similarity 49.3%; Pred. No. 3.3e-79;
Matches 360; Conservative 118; Mismatches 162; Indels 90; Gaps 19;

QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPQIAMFCGRLLMHMHVQNGKWDSDP 56
Db 15 LLLVLLGLTAPAAALAGVIEAALANAGTGFAVAEPQIAMLCGLKLMHMHVNIQTCKWEDP 74
QY 57 SGTKICIDTKEG;LQYQCEVPELOITNVNANQVPTIQNMCKRGKCKOCKTHPHVPIYR 116
Db 75 TGTGKSLGTEEVLYQCEIYPELQITNVMEANQPVNDSMCRDRCKRCKS--HIVIPFK 132
QY 117 CLVGEFVSALLVPCKKFLHQRMDVCEITHLWHITVAKETCSEKSTNLHRYGMLPCGI 176
Db 133 CLVGEFVSIVLLVPNCQFFHQHMEVCEKHORHITLVKEACLTGLTLYSGMLPCGV 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEDSDVMWGGADTGYAGSSEKVVVEVAE---E 231
Db 193 DQFHGT;EYVCCPQTKTVSDSTNSKEFEDEE-----DEEEDFYDLCKSEFTE 243
QY 232 EIVAEEVEEAD--DDEDDGDEVEEEAE-----EPYEEATERT;SIAITTTTIES 282
Db 244 ADUEDTEAAADEEEDDEEVEVEDRDYDYDPKGGDYN--ENPTPSEGTISDKE 301
QY 283 VERVVRVPTAASITPAVDKYLETQDENEHAFQKAKERLEAKRERMSQVMREWEPAE 342
Db 302 IVHDVKVPT;PLPTND--VDVYLETSAADDNEHARFQAKHOLEIRHRNRMDRVKKEWEPAE 360
QY 343 HQAKNLPKADKKAVIOHFOEKVESLEQEAANEQQVLVETHMARVEAM;NDRRRLALENYI 402
Db 361 LQAKNLPKTERQTIQHFOAKYKAEKAAASEKQQLVETHLAKVEAMLNDRRR;ALENYL 420
QY 403 TALQAVPRPRHIVFNMLKKYVRARQKDRQRTLKHEHVRKVDPKKAQAQIRSOVMTHLRVI 462
Db 421 AALQSDPPRHR;LQAI;RKYVRAENKDRLHTIRHYOVLAVDPEKAAQMKSOVMTHLVI 480
QY 463 YERMNOSLSL;NVF;AVAEIODEVDEILQKEUNYSDVVIANKIPEPRISVNDALMPSL 522
Db 481 EERRNQSLLYKVPVVAQEIODEIDELLQEQR-----ADM-----DOFISII 523
QY 523 TERKTTVELLPVNGEESDLOLPWHSFGADSVANTENEVEPVDARPAADKGLTIRPGSG 582
Db 524 SENPVDVRSSEKSE-EIPFFPLHPF-----PSUSENE-----GSGMAEQDQ-G 566
QY 583 LTNIKITEEI-SEYKMDAEFRHDSGVVHHQKLVFFAEDVGS-----NK 624
Db 567 LIGAEKVINSKNKMDENNVIDETLDV--KEMIFNARVGGLEEBEPESVGPLREDFSLSS 624
QY 625 GATIGLMVGQWIATVIVITLVMLKKQYTSIHGGVVEVJAAVTPERHLSKMQNGVYEN 684
Db 625 NALIGLLVIAVAIATVIVISLVMLRKQYGTISHGIVEVDPMLTPEERHLNKNQNGYEN 684
QY 685 PTYKFFEQMQ 694

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DB      635 PTKYLECQM 694
||||| |||
RESULT 9
APP2.HUMAN
ID APP2.HUMAN STANDARD: PRT: 763 AA.
AC Q06481.
DI 01-JUN-1994 (Rel. 29, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE (CDEI-box binding protein) (CDBBP).
GN APLP2 OR APLP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93250009; PubMed=8495127;
RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA Norris K., Foster D.C.;
RT "Molecular cloning of the cDNA for a human amyloid precursor protein:
RT homolog; evidence for a multigene family.";
RL Biochemistry 32:4481-4486(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Hanes J., Klaudiny J., Schreit K.H.;
RT "A human amyloid precursor-like protein is highly homologous to a
RT mouse sequence-specific DNA-binding protein.";
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035131; PubMed=8220435;
RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA Hyman B.T., Neve R.L., Tanzi R.E.;
RT "Isolation and characterization of APLP2 encoding a homologue of the
RT Alzheimer's associated amyloid beta protein precursor.";
RL Nat. Genet. 5:95-99(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Huotow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaeetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Kaha S.S., Loquellanc N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gnaratine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Ketteran M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Houffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grummet J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 5,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC MAY BIND TO THE DNA 5'-GTACATG-3' (CDEI BOX).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR

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Query Match      47.3%; Score 1728; DB 1; Length 763;
Best Local Similarity 47.1%; Pred. No. 8,1e-79;
Matches 372; Conservative 112; Mismatches 165; Indels 140; Gaps 20;

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FT CONFLICT 575 577 /FTID-VSP_000021.
FT SEQUENCE 765 AA: 86882 MW: CF51PCCCE30SAQCE CRC64:
SQ
Query Match 47.0%: Score 1716; DB 1: Length 765;
Best Local Similarity 46.2%: Pred. No. 3,26-78;
Matches 364; Conservative 122; Mismatches 166; Indels 136; Gaps 20;
QY 5 LALLLLAAWTARALEV-----FTDGNAG---LLAEPOIAHKCGRLNHHMNVCKNKKLSDP 56
DB 15 LVVLLGLTAAALAGYIEALANAGTGFAVAEPQIAFCGKLNMEVNTCTGRKAFDP 74
QY 57 SGTICIDTKEGILQYCEVYPELQITNVZPANGPVTIQNMCKKRGKCKTHPFEVPIYK 116
DB 75 TGTSCSLCTKEVLQYCEVYPELQITNVZPANGPVTIQNMCKKRGKCKTHPFEVPIYK 116
QY 117 CLVGEFVSALLVPDKKFLHQERMDVCEETHLHHTYVAKESCSSEKSNLHEDYGMJLPGY 176
DB 133 CLVGEFVSALLVPDKKFLHQERMDVCEETHLHHTYVAKESCSSEKSNLHEDYGMJLPGY 176
QY 177 DKFCVGVVCCPLAE--ESDNNVSADAEEDSDVKNMGADTDYA-DGSEDKVVEVVAPEER 233
DB 193 DQFPGTVEVCCPOTKVVDSDSMTKKEKEFEFE-----DEEDYALDKSEPTHEADLFTT 248
QY 234 VAEVEEESADDEDDEDGEVEEAEPEYEE-----AETRTSTATTITTTESVEEVV 287
DB 249 EAAADEDEFEFEFEVEEVEEDDYDYUSFKGIDVNEENPTPESSDGTISDKEFAHGV 308
QY 288 R-----VPT 292
DB 309 KAVCSQEAHTGPCRAVMPRWYEDLSKGVRFYGGCGGNRNFESENYCMVAGTKTIPP 368
QY 292 TAASTPDVADVKYLETPGDENEHAFQAKAKEMIAKHHRMSQVMRENEFAERQAKNLPKA 352
DB 369 TPLPIND-VNYFEISADNEHAFQAKAKEMIAKHHRMSQVMRENEFAERQAKNLPKA 427
QY 352 DKKAVIQHFQKVESLEQEAANERQOLVETHHARVEAMLNDRRLALZENYITA-QAVPPR 411
DB 428 BROTLIQHFOAMVKALEKFAASEKQQLVETHLARVEAMLNDRRLALZENYITA-QAVPPR 487
QY 412 PRHVNMLKVVYRAOKDROHTLKHFEHVRVMDPKAAQIRSOVMTHLRVIYEBNOSLS 471
DB 488 PHRLQALRRVYRAENKDRHLHRIHQHVLAVDEPKAAQMSQVMTHLRVIYEBNOSLS 547
QY 472 LYNYPAVAEEIQDEVDLLOKEQNYSDVLANNMISEPRIISYGNDAALMPSLITE:KTVTEL 531
DB 548 LLYKVPYVAEQIEEIDELQEQR-----ADM-----DOFTSSISENPVDVR- 599
QY 532 LPVNGEFLDLOPHWSTGADSVFANTENEVEPYDAPADRGLTTRPGSLTN-----I 596
DB 590 --VSSSES-EEIPFPHP--HPFFSLSENE-----DTQPELYHPM--KKGSCMAEQDGLIT 638
QY 587 KTEE---ISEVKMAEPRHDSGYEVHHOKLVFFAEEDVGS-----NKGK 626
DB 639 GAEEKVINKKNKKNENWVYDTELAV-KEMFNARVKGLIEEEDSVGLPREDVSLSSA 696
QY 627 IGLMGVGVATVITVITLVMLKKKQYTSIHGGVVEVZAAVYPEERHLKSKQOQNSYENPT 696
DB 697 LIGLIVIAVAIATVIVISVLMRLKQYGTLSHGIVEVHPMLTPEERHLKKNQNHGYNPT 756
QY 687 YKFEQCMQ 694
DB 757 YKYLFOQM 764

```

RESULT 11

APPL_HUMAN

ID APPL_HUMAN STANDARD: PRI: 650 AA.

AC P51693; O00113; Q96A92;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Amyloid-like protein 1 precursor (APLP-1) [Contains: C30].

```

GN APPL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
[1]
RX SEQUENCE FROM N.A.
MEDLINE=98088960; PubMed=9428684;
RA Paliga K., Peraus G., Kreyer S., Duwrrwang U., Hesse L., Muthaup G.,
RA Masters C.L., Beyreuther K., Weidemann A.;
RA "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
RA expression in COS-7 cells and identification of soluble forms in the
RA cerebrospinal fluid.";
RA Eur. J. Biochem. 250:354-363(1997).
RN [2]
RX SEQUENCE FROM N.A.
MEDLINE=98180887; PubMed=9521586;
RA Lenkkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
RA Olsen A., Tryggvason K.;
RA "Structure of the human amyloid-precursor-like protein gene APLP1 at
RA 19q13.1";
RA Hum. Genet. 102:192-196(1998).
RN [3]
RX SEQUENCE FROM N.A.
TISSUE=Ovary;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold F.A., Grouse L.H., Dergo J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hirschman R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Schevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RX POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
MEDLINE=96115107; PubMed=7494461;
RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
RA Black I.B.;
RA "Selective localization of amyloid precursor-like protein 1 in the
RA cerebral cortex postsynaptic density.";
RA Brain Res. Mol. Brain Res. 32:36-44(1995).
RN [5]
RX HEPARIN AND ZINC BINDING.
MEDLINE=95014513; PubMed=7929392;
RA Bush A., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RA "The amyloid beta-protein precursor and its mammalian homologues.
RA Evidence for a zinc-modulated heparin-binding superfamily.";
RA J. Biol. Chem. 269:26618-26621(1994).
RN [6]
RX INTERACTION WITH APBA2.
MEDLINE=99107877; PubMed=9890987;
RA Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA Sakiyama S., Kirino Y., Suzuki I.;
RA "Interaction of a neuron-specific protein containing PDZ domains with
RA Alzheimer's amyloid precursor protein.";
RA J. Biol. Chem. 274:2243-2254(1999).
RN [7]
RX EXTRACELLULAR COPPER-BINDING.
MEDLINE=22130992; PubMed=12135352;
RA Simons A., Ruppert T., Schmidt C., Schlicksupp A., Fipkorn R.,

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APPL_MOUSE STANDARD; PRG: 653 AA.
AC 003157; Q8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DI 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN APLP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=93065322; PubMed=1279693;
RA Wasco W., Bupp K., Magendanz M., Gusella J.F., Tanzi R.E.,
RA Solomon F.;
RP SEQUENCE-BRAIN;
RC TISSUE-Brain;
RX MEDLINE=93065322; PubMed=1279693;
RA Wasco W., Bupp K., Magendanz M., Gusella J.F., Tanzi R.E.,
RA Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10759-10762(1992);
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Retina;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse J.H., Dege J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Sherman C.M., Schrier G.D.,
RA Atschul S.P., Zeeberg B., Huotow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Malishy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.C., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Li X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN [3]
RP COLLAGEN-BINDING.
RX MEDLINE=96139497; PubMed=8576160;
RA Behr D., Hesse I., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996);
RN [4]
RP INTERACTION WITH DAB1.
RX MEDLINE=99389880; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT protein 1.";
RL J. Neurosci. 13:7507-7515(1999);
RN [5]
RP INTERACTION WITH MAPK8IP.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Hemma Y., Ito Y., Niikura T., Hitaki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001);
RN [6]
RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
RP TYR-641.
RX MEDLINE=22313598; PubMed=12228233;
RA Scheinfeld M.H., Chersi E., Laky K., Fowkes B.J., D'Adamo L.;

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RT Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT secretase regulates transcription.;
RL J. Biol. Chem. 277:44195-44201(2002).
CC !- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALD1, activates transcription
CC activation through APBB1 (Fe65) binding. Couples to JIP signal
CC transduction through C-terminal binding. May interact with
CC cellular G-protein signaling pathways. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I.
CC !- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).
CC !- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB and APBA family members, its
CC MAPK8IP1 and Dab1 (by similarity). Binding to Dab1 inhibits its
CC serine phosphorylation.
CC !- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.
CC !- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clathrin-mediated
CC endocytosis.
CC !- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC similarity).
CC !- PTM: N-glycosylated.
CC !- PTM: O-glycosylated.
CC !- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.
CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L04538; AAA37247.1;
DR EMBL: BC021877; AA821877.1;
DR PIR: A46362; A46362.
DR HSP: P05067; LMWP.
DR MGD: MGI:88046; Aipl1.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW Glycoprotein.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 553 AMYLOID-LIKE PROTEIN 1.
FT DOMAIN 624 553 C30 (BY SIMILARITY).
FT TRANSMEM 38 583 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 594 606 POTENTIAL.
FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 157 177 COPPER-BINDING.
FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 263 271 POLY-GLU.
FT DOMAIN 535 538 POLY-SER.
FT DOMAIN 501 606 POLY-LEU.
FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY

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DB 6 LMIGLLIPILVA-TVYAEAGSPAGSKRHEKEIFPMVAFSGYRNQYM-TEEGSKTKDDEHYA 63
QY 61 TCIDIKEGILQYCEVPELOITVWVEANQPVTTQWCKRGRKCKCKTHPRVIVIPRCLVG 120
DB 64 TCFSGKDLILKCYKAPSMNITIVESVHSVSOMCREGSPCK-WTHSVRYPHGIDG 122
QY 121 EFVSADLLVPCKAFKFOERMDVCEHLHWHVTVAKETCSEKSTN-----LHDYGMGLLPC 174
DB 123 EFHSEALVPHDCQFHSVNSQCNDQYHWDKAGCKCKTKSKGNKDMIVKSFVAVLPC 182
QY 175 GIDPRGVFVCCPLAESDNVDSADAEEDSDVWVGADPYADGSPCKVVEAEFEV 234
DB 183 ALDMFIFGVFVCCP-----NDQTNKTDVOKTK----- 209
QY 235 AEVEEEAADDDEDDGDEVEEAEPEYEPATERTISATTTITTSVEVVRVPTTAA 294
DB 210 ---EDDDGDDDDDAYEDDYSEEDKDEE----- 236
QY 295 STPDVADKYLETPGDENEHAHFQKAKERLEAKHRMSQVWKEFEA-----EPOAKNLP 349
DB 237 -EPSSQDPYFIANWINEHDDFKAEHMDKHKYDKVKNKGWDLTRVNEOKAKD-P 294
QY 350 KADKKAVQ---HFQEKVESLEQEAANEROOLVETHMARVAMLNDRRRCALFNITAL- 405
DB 295 KGAEFKFSQMARPOKTVSSLEEDHKRMRKEIEAVHEERVOAMLEKKRSDATHDYKQALA 354
QY 406 -QAVPPRPHVENMLKKYVRAEQDROHTLKHFEHVRMVPDKKAAQ-PSQVWTHLAVYE 464
DB 355 THVKNPKNHSVLOS-KAVIRAEEDKDRMHTLNKYLKADSKAEAAVKTIVHRIKTYIDL 414
QY 465 RINOSLSLLYNP-----AVA--FEIQDEVZELIQFQNYSDUOLANKTSEPRISY 513
DB 415 RINGTLAMLRDEPDKLVYRPIANTYKNKYDEVSPOISVE---DSELTPLHDEDFSK 470
QY 514 GN--DALMPSLT-----EKTIVVELLPVNGFSLDQLQWHSFGADSVPAWT---ENEVPE 564
DB 471 NAKLDVKAPTITIAKPVKETDNKVLPT'EASDSEEEADYDEDEDEQVKKTPDKKKVKV 530
QY 565 VDARP-----AADRLTTPGSGSLNITEE-----ISEVKMDA 596
DB 531 VDIPKELKVITIEKKAPKLVETSVQTDDEDDSSSTSESDDEDKNKKELRVET 590
QY 599 E-----FRHDSGVEVHHQKLVFAEDVGSNKGAIGIIMVGGVVATVIVITLVMLK 649
DB 591 EPIIDEPASFYRHD-----KLIQSPVEVSASSVFPQVVLASAMFITAICILIAFAT 642
QY 650 KKQVTSIHGVVEVDAAVTPERHLSKMQQNGYENPTYKFFE 591
DB 643 NARRRRAMRGFIEVD-VYTPERHVAGVQNGYENPTYSFED 583
RESULT 14
AA_IDROME STANDARD; PRT; 897 AA.
AC P14599; Q91VW0; Q9U4H3; Q9W5F1;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-amyloid-like protein precursor.
GN APPL OR VND OR BCDNA:GH0413 OR EG:65F1.5 OR CG7727.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea; Drosophilidae; Diptera; Brachycera; Muscomorpha;
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69184650; PubMed=2434667;
RA Rosen D.R., Martin-Norris L., Luo L., White K.;
RI "A Drosophila gene encoding a protein resembling the human
RL beta-amyloid protein precursor.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrall B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Urquano S., Gloux S., Lelaure V., Mottier S., Galibert F., Rorkova D.,
RA Papaannakis G., Spanos L., Cox S., Siden-Kiamos I., Bolshakov S.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell I.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Vaienti P., Saunders R.D.C.,
RA Glover D.M.;
RI "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster.";
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Borman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale K.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RI "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review.";
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrall B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Urquano S., Gloux S., Lelaure V., Mottier S., Galibert F., Rorkova D.,
RA Papaannakis G., Spanos L., Cox S., Siden-Kiamos I., Bolshakov S.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell I.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Vaienti P., Saunders R.D.C.,
RA Glover D.M.;
RI "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster.";
RN [5]
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RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Paels B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith I.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RI "The genome sequence of Drosophila melanogaster.";
RN [3]
RP REVISIONS.
RX STRAIN=Berkeley;
MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Borman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale K.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RI "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review.";
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Oregon-R;
MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrall B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Urquano S., Gloux S., Lelaure V., Mottier S., Galibert F., Rorkova D.,
RA Papaannakis G., Spanos L., Cox S., Siden-Kiamos I., Bolshakov S.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell I.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Vaienti P., Saunders R.D.C.,
RA Glover D.M.;
RI "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster.";
RN [5]
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RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Ovary;
RA MEDLINE=20196012; PubMed=10731138;
RX Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
RA Stapleton M., Harvey D.A.,
RT "A Drosophila complementary DNA resource";
RJ Science 287:2222-2224 (2000).
RN [6]
RP SEQUENCE OF 1-83 FROM N.A.
RX MEDLINE=91184006; PubMed=2127912;
RA Martin-Morris L.E., White K.;
RT "The Drosophila transcript encoded by the beta-amyloid protein
RJ precursor-like gene is restricted to the nervous system";
RJ Development 110:185-193 (1995).
CC -!- FUNCTION: Probably corresponds to the protein encoded by the
CC essential locus vnd, a gene required for embryonic nervous system
CC development.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in post-mitotic neurons in the
CC central and peripheral nervous systems. Within the nervous system
CC transcripts are not observed in neuroblasts, newly generated
CC neurons and at least one class of presumed glia cells.
CC -!- DEVELOPMENTAL STAGE: Expressed in all developmental stages.
CC -!- DOMAIN: The clathrin-binding site is essential for its association
CC with alpha-, beta-, and gamma-. The sequence specific
CC recognition extends to peptide residues that are C-terminal to the
CC NPXY motif. This interaction appears to be independent of
CC phosphorylation (By similarity).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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DR EMBL; J04516; AAA28874.1; .
DR EMBL; AF003418; AAF45520.2; .
DR EMBL; AF0031883; CAA21409.1; .
DR EMBL; AL022139; CAA21409.1; JOINED.
DR EMBL; AL022139; CAA18093.1; .
DR EMBL; AL031883; CAA18093.1; JOINED.
DR EMBL; AF181628; AAC55414.1; .
DR EMBL; X55774; CAA39294.1; .
DR EMBL; X55775; CAA39294.1; JOINED.
DR PIR; A32758; A32758.
DR HSP; P05067; 1IMP.
DR
DR GO; GO:0005576; C:cytoplasmic; IDA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR InterPro; IPR001968; A4_APP.
DR Pfam; PF02177; A4_EXTRA; .
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal; Transmembrane; Amyloid; Neurogenesis.
FT SIGNAL 1 27
FT CHAIN 28 887
FT DOMAIN 28 813
FT TRANSMEM 814 834
FT DOMAIN 835 887
FT DOMAIN 877 880
FT CARBOHYD 150 150
FT CARBOHYD 161 161
FT CARBOHYD 237 237
FT CARBOHYD 240 240
FT CARBOHYD 574 574
FT CONFLICT 177 177
FT CONFLICT 229 229
FT CONFLICT 332 332
FT CONFLICT 743 743
FT S -> T (IN REF. 1).
FT MISSING (IN REF. 1).
FT V -> M (IN REF. 4).
FT S -> T (IN REF. 1).

SO	SEQUENCE	887 AA:	98332 MW:	P0F0855AD65A5275	CRCS4;
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	Best Local Similarity	25.5%;	Pred. No. 3.8e-30;		
	Matches 233;	Conservative 128;	Mismatches 287;	Indels 265;	Gaps 25;
QY	7	ILLANNTARALEVPTGAGLLA----	EPQIATYC--GRLNHNMY--QNGKWDSDPS;	58	
DB	9	ILLRSWVLA-----CTAQVAAAPRWEPTAVLCAGQIYQPYLSEPRGWVLDL	SK 63		
QY	59	2---KICDTEKIGLOXCOEYVPELQITNVVEANOPVTLQNMCKRG---	RKCKTHTHFV 112		
DB	64	KTGPTCLRDYKVDLLDYCKKAYPNKDTNIVESHYKIGGWCAGALNAKCKGSIRMI	123		
QY	113	IPYCLVGVFSDALVDFKCKFLHQBEMDVCEPHLHMHTVAKETCEKTNJHDYGMLL	172		
DB	124	KPFRCL--GPFOSDALLVPEGLFDH1HNASRCMPFVWNTGAAACOERGMQRSEFAMLI	182		
QY	173	PCGTDKRGVEVCCP-----	LAFESDNDV---S 198		
DB	193	FCGLSVFSGVEVCCPKFKTKDEIHWKIDLPVMPAAQINSANDELVMNDEDDSNUSNY	242		
QY	199	ADAEEDSDVMWGADTGYADGSEDKYVEVAEEV-----	AE 236		
DB	243	KDANEDDLJ-----DEDDLMDDEDDMDVADEAATAGGSPNTGSSGSDSLDOINAE	296		
QY	237	VEE--PEADDDDEDDGDEVEEAEPEY-----	EEATER 268		
DB	267	YDSGEYNYEDGAGSEAEVSEASDQSGGAKVSLKSDSSPSPAPVAPAEKAPVK	356		
QY	269	TTSATITTTTTEVEEV-----RVPTTAASIPDAVDKYLETFCDENEHAHFQ	317		
DB	357	SESVTSTPOLSASAAAFVAANSNGSGTGAGAPPSTAQTS---DPVTFHDPHYEQSYK	413		
QY	318	KAKELEKAKPERMSOYMRWEAEAEAKNLPKADKA-----VIOHFQEKVESLEQE	370		
DB	414	VSOKRESHREKVTIRYKOWMSLEEKYQDMRLADPRAAQSFQRMWTFQTSVQALEEE	473		
QY	371	ANERQQLVETHMARVEAMLRRLALENYITLQAVPPRPRHVFNMLKKYVRAEKDR	430		
DB	474	GNAEKHQLAAMHQORVLAHINORKREAMTCYQALTEOPNNAHVEKCIQKLLRALHKDR	533		
QY	431	QHTLKHFEH--VRMVDP---KKAQIRSOVMTHLVIYERKNQSLSLLYNYPVAEEI---	483		
DB	534	AHALAHYHLLNSGCGPGGLEAAASERPRIERLIDIDRAVNSQMTMLKRYFELSAQOL	593		
QY	484	-----QDEV-----	487		
DB	594	KNDYILALRSKDDINGSSLSGMEAEAGILDKYRVEIKRYAEKURLAEKORKEQRAA	653		
QY	488	-----DELIOKEQNYSDDLANWIS-----	FRISYGNIAL 518		
DB	654	EKEKLEEKLRLEAKKVDMLKSOVAFQSOPTOSSTQSOAQOQOQPKSLPGKELGPDAA	713		
QY	519	M-----PSLIEIKTTVEILLPVNGEFSLDLOPHMSFGADSVFPAANTEVEFVDARPAADR	573		
DB	714	LVIAANPNLE--TKS-----EKDLSDE-----YGEATVSSTKVOTVLTPTVDDDAVQR	760		
QY	574	SLTTPGSGLNINIKTEIESEVKMAEFHDSGVEYHHQKLVF-----PAEDVSNK---G	625		
DB	761	AVEDVAAA-----VAHQEAEPQVQHFMTHDLGHRESSFSLRRREFAQHAHAAKEGRN	811		
QY	626	ATIGLVGGVWVATVIVITLVKLKKKQVTSIH--HGVVEVDAAVTP-----EERHLSKMQ	678		
DB	812	VYTFISFAGIALMAAFVGVAVAKWRTSRSPHAQGFTEVDQNVTTTHPIVREKIPVNMQ	871		
QY	679	QNGYENPYKFFE 691			
DB	872	INGYENPYKFE 884			

RESULT 15
A4_BOVIN

```
ID A4_BOVIN STANDARD: PRT: 59 AA.
AC Q28053;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.B., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC !- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
CC !-
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC !-
CC EMBL: X56124; CAA39589.1; -
CC EMBL: X56126; CAA39591.1; -
CC HSP: P05087; IBA4.
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF03494; Beta-APP; 1.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 56 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SQ SEQUENCE 59 AA: 6414 MW: F43469D488A2E12D CRC64:

Query Match 8.0% Score 292; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 591 ISEVKMDAEFRHDSGVEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA:VIVITLVMLK 649
DB 1 ISEVKMDAEFRHDSGVEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA:VIVITLVMLK 59
```

Search completed: October 2, 2003, 13:59:35
Job time : 15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM: protein - protein search, using sw model

Run on: October 2, 2003, 13:56:24 ; Search time 39 Seconds
(without alignments)
4611.863 Million cell updates/sec

Title: US-09-806-194-16

Perfect score: 3651
Sequence: 1 MLPGIALLLAAWTARALEV.....OONGYENTYKFFEQMKNK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052504 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

Database: SPTREMBL23:

- 1: sp.archaea:
- 2: sp.bacteria:
- 3: sp.fungi:
- 4: sp.human:
- 5: sp.invertebrate:
- 6: sp.mammal:
- 7: sp.mhc:
- 8: sp.organelle:
- 9: sp.phage:
- 10: sp.plant:
- 11: sp.rodent:
- 12: sp.virus:
- 13: sp.vertibrate:
- 14: sp.unclassified:
- 15: sp.virus:
- 16: sp.bacteriap:
- 17: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DR	ID	Description
1	3573	97.9	695	11	Q60496	Q60496 cavia sp. p
2	3340	97.0	695	11	P97487	P97487 mus musculu
3	3535.5	96.8	770	6	Q9TU10	Q9TU10 sus scrofa
4	3428	93.9	695	13	Q9PGJ8	Q9PGJ8 gallus gall
5	3387	92.8	751	13	Q9DGL7	Q9DGL7 gallus gall
6	3214	88.0	693	13	Q9SGG0	Q9SGG0 xenopus lae
7	3190	87.4	695	13	Q9SFF9	Q9SFF9 xenopus lae
8	3103	85.0	747	13	Q91963	Q91963 xenopus lae
9	2964.5	81.2	599	13	Q57394	Q57394 narke japon
10	2767.5	75.8	569	13	Q9PVL1	Q9PVL1 gallus gall
11	2635.5	72.2	607	11	Q99K32	Q99K32 mus musculu
12	2613	71.6	534	13	Q93296	Q93296 gallus gall
13	2573	70.5	780	13	Q73683	Q73683 tetradon f
14	2529	69.3	738	13	Q90W28	Q90W28 brachydario
15	2487.5	68.1	694	13	Q8UUR9	Q8UUR9 brachydario
16	2448.5	67.1	737	13	Q93279	Q93279 fuqu rubrip

17	2339	64.1	612	13	Q919E7	Q919E7 brachydario
18	1928	52.8	384	11	Q8BPC7	Q8BPC7 mus musculu
19	1762	48.3	695	4	Q13861	Q13861 homo sapien
20	1749.5	47.9	669	4	Q14662	Q14662 homo sapien
21	1740	47.7	695	11	Q64348	Q64348 mus musculu
22	1708	46.8	763	11	Q61482	Q61482 mus musculu
23	1704	46.7	751	11	Q60709	Q60709 mus musculu
24	1655	45.3	472	13	Q8UUS0	Q8UUS0 brachydario
25	1350.5	37.0	357	13	Q8UUI8	Q8UUI8 brachydario
26	1301.5	35.6	522	4	Q9BT36	Q9BT36 homo sapien
27	1090	29.9	218	11	Q8BPV5	Q8BPV5 mus musculu
28	1048.5	28.7	523	4	Q14594	Q14594 homo sapien
29	771	21.1	239	13	Q8UUI7	Q8UUI7 brachydario
30	678	18.6	136	6	P79307	P79307 sus scrofa
31	577	15.8	113	13	Q8JH58	Q8JH58 chelydra se
32	561	15.4	182	11	Q9CYS4	Q9CYS4 mus musculu
33	478	13.1	97	6	Q28673	Q28673 oryctolagus
34	393.5	10.8	82	4	Q16019	Q16019 homo sapien
35	389.5	10.7	82	4	Q16014	Q16014 homo sapien
36	387.5	10.6	82	4	Q16020	Q16020 homo sapien
37	376	10.3	79	11	Q35463	Q35463 cricetus
38	358.5	9.8	160	11	Q9QZ78	Q9QZ78 cavia sp. p
39	335	9.2	208	11	Q8R0R7	Q8R0R7 mus musculu
40	239	6.5	49	6	Q97917	Q97917 bos taurus
41	196.5	5.4	727	5	Q95TC7	Q95TC7 drosophila
42	196.5	5.4	5303	5	Q9V628	Q9V628 drosophila
43	193	5.3	785	5	Q9GQ82	Q9GQ82 drosophila
44	192.5	5.3	556	5	Q9S593	Q9S593 drosophila
45	192.5	5.3	1110	13	Q91255	Q91255 petromyzon

ALIGNMENTS

RESULT 1

Q60496	PRELIMINARY:	PRT:	695 AA.
10	Q60496		
AC	Q60496:		
DI	01-NOV-1996 (TRENBLrel. 01, Created)		
DI	01-NOV-1996 (TRENBLrel. 01, Last sequence update)		
DI	01-OCT-2002 (TRENBLrel. 22, Last annotation update)		
DE	Putative amyloid precursor protein.		
OS	Cavia sp.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.		
OX	NCRI_TaxID=10143;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=97236426; PubMed=9116031;		
RA	Beck M., Mueller D., Bigl V.;		
RI	"Amyloid precursor protein in Guinea pigs - complete cDNA sequence and alternative splicing.";		
RI	Biochim. Biophys. Acta 1351:17-21(1997).		
DR	EMBL; X97631; CAA66230.1; .		
DR	HSSP; P05067; 1BA4.		
DR	InterPro; IPR001868; A4_APP.		
DR	InterPro; IPR001255; Beta_APP.		
DR	Pfam; PF02177; A4_EXTRA; 1.		
DR	Pfam; PF03494; Beta_APP; 1.		
DR	PRINTS; PR00203; AMYLOIDA4.		
DR	SMART; SM00006; A4_EXTRA; 1.		
DR	PROSITE; PS00039; A4_EXTRA; 1.		
DR	PROSITE; PS00320; A4_INTRA; 1.		
SQ	SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;		

Query Match	97.9%;	Score 3573;	DB 11;	Length 695;
Best Local Similarity	97.8%;	Pred. No. 2.7e-207;		
Matches 680;	Conservative 6;	Mismatches 9;	Indels 0;	Gaps 0;
Qy	1	MLPGIALLLAAWTARALEVPTDGNAGLAEFPQIAMFCGRLLNMHMVQNGKWDSPSGTK	60	
Db	1	MLPSIALLLTTTARALEVPTDGNAGLAEFPQIAMFCGRLLNMHMVQNGKWEFDPSTGK	60	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RV SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.:
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -;
DR HSSP: P05067; IAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPT1.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPT1; 1.
DR PRINTS: PR00759; BASICTASE.
DR PRODOM: PD000222; Kunitz_BPT1; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE: PS0279; BPT1_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86% MW; 5F7A1DCR2BC583E CRC64;

Query Match 96.8%; Score 3535.5; FN 6; Length 770;
Best Local Similarity 88.4%; Pred. No. 5.6e-205;
Matches 581; Conservative 8; Mismatches 6; Indels 75; Gaps 1;
QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPTQAMFCGRNLNHHMNVQNGKMSDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPTQAMFCGRNLNHHMNVQNGKMSDSPSGTK 60
QY 61 TCIDTKESILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYRCLVG 120
DB 61 TCIDTKESILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
DB 121 EFVSDALLVPDKKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
QY 181 GFVFCCPLAESDNVDSADAEEDSDVWVGADYDADGSDKVEEVEEYVR 288
DB 181 GFVFCCPLAESDNVDSADAEEDSDVWVGADYDADGSDKVEEVEEYVR 288
QY 289 ----- 288
DB 301 RMLSRWYFDVTEGKAPPTFGGGGNRNFDTVEEYCMVCGSVMSGLLKTTQHLPOD 360
QY 289 ---YPTIAASTPAVDKYLETIPGDENEHAHFQKAKERLEAKHRERMSQVREAEERCA 345
DB 361 PVKLPPTAASTPAVDKYLETIPGDENEHAHFQKAKERLEAKHRERMSQVREAEERCA 420
QY 346 KNLPKADKAVIQHFQKVESLQEAANERQQLVETHMARVEAMLNDRRLALENTAL 405
DB 421 KNLPKADKAVIQHFQKVESLQEAANERQQLVETHMARVEAMLNDRRLALENTAL 480
QY 406 QAVPRPRPHVFMKKYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSQVMHLRVIYER 465
DB 481 QAVPRPRPHVFMKKYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSQVMHLRVIYER 540
QY 466 MNQSLSLYNPVAAEIQDEVDLQEQNYDDVLANNISPRISYGNDA:MPSLIET 525
DB 541 MNQSLSLYNPVAAEIQDEVDLQEQNYDDVLANNISPRISYGNDA:MPSLIET 600
QY 526 KTIIVELLPVNGEFLDQLQFWHSGADSVPAANTENEVEPVDARPAADRGJITRPGSGLTN 585

DB 601 KTIIVELLPVNGEFLDQLQFWHSGADSVPAANTENEVEPVDARPAADRGJITRPGSGLTN 660
QY 586 KTEIEISFVKMDAEFRHDSGYEVHOKIVFAEDVGSNGKGAIIICIMVGGVVIATVITL 645
DB 661 IKTEIEISFVKMDAEFRHDSGYEVHOKIVFAEDVGSNGKGAIIICIMVGGVVIATVITL 720
QY 646 VMLKKQVTSIHGQVVEVDAVTPERRHLSKMQONGYENPTYKFFEQMQN 695
DB 721 VMLKKQVTSIHGQVVEVDAVTPERRHLSKMQONGYENPTYKFFEQMQN 770
RESULT 4
Q9DQJ8 PRELIMINARY; PRI: 695 AA.
AC Q9DQJ8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodosse A., Sorribas V.:
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAG00593.1; -;
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00263; AMYLCIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC54;
Query Match 93.9%; Score 3428; DB 13; Length 695;
Best Local Similarity 94.0%; Pred. No. 1.5e-198;
Matches 655; Conservative 17; Mismatches 21; Indels 4; Gaps 3;
QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPTQAMFCGRNLNHHMNVQNGKMSDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPTQAMFCGRNLNHHMNVQNGKMSDSPSGTK 60
QY 61 TCIDTKESILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYRCLVG 120
DB 61 TCIDTKESILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
DB 121 EFVSDALLVPDKKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
QY 181 GFVFCCPLAESDNVDSADAEEDSDVWVGADYDADGSDKVEEVEEYVR 238
DB 181 GFVFCCPLAESDNVDSADAEEDSDVWVGADYDADGSDKVEEVEEYVR 240
QY 239 EEEADDDDEDGDEVEEAEPEYEATERTTSIATTTTTSVEEVVPTAASIPD 298
DB 241 DEDADDDDDDDGDEI-EETEEVEEATERTTSIATTTTTSVEEVVPTAASIPD 298
QY 299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVREAEERCA:PKADKAVIQ 358
DB 299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVREAEERCA:PKADKAVIQ 358
QY 359 HFQKVESLQEAANERQQLVETHMARVEAMLNDRRLALENTALQAVPPRPHVFM 418
DB 359 HFQKVESLQEAANERQQLVETHMARVEAMLNDRRLALENTALQAVPPRPHVFM 418

```

Db 359 HFGEKVESLEQSAAREKQJLVETHMARVEAMLNDRKRIALENYITATQTVPPRPHVFN 478
QY 419 LKYYRAEOKDQROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPA 478
Db 419 LKYYRAEOKDQROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPA 478
QY 479 VAEETODEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTIVVELLPVNGCF 538
Db 479 VAEETODEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTIVVELLPVNGCF 538
QY 539 SLEDDQPHKSFCAQSVNPANTENEVEPVDARPAADRGHTIRPGSGLIN:KTFEISEVKMCA 598
Db 539 SLEDDQPHKSFCAQSVNPANTENEVEPVDARPAADRGHTIRPGSGLIN:KTFEISEVKMCA 598
QY 599 EFRHDSGVYVHHQKLVFFAEIDVGSNGKAIIGLMVGQVVIATVITLVN:KKKQYTSIEH 659
Db 599 EFRHDSGVYVHHQKLVFFAEIDVGSNGKAIIGLMVGQVVIATVITLVN:KKKQYTSIEH 659
QY 659 GYVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMGN 695
Db 659 GYVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMGN 695

RESULT 5
QSDGJ7
ID QSDGJ7 PRELIMINARY: PRT: 751 AA.
AC QSDGJ7
DI 01-MAR-2001 (T-EMBLrel. 16, Created)
DI 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DI 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolase A., Sorribas V.:
RT *Cloning of full-length chicken beta-amyloid precursor protein:
RT isoforms.
RJ Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289219; AAG00594.1;
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00014; Kunitz_BPTI; 1.
DR PRINTS: PR02023; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASP.
DR ProDom: PD00222; Kunitz_BPTI; 1.
DR SMART: SM00306; A4_EXTRA; 1.
DR SMART: SM00331; Kunitz; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_Kunitz_1; 1.
DR PROSITE: PS02079; BPTI_Kunitz_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA: 64705 MW: 87894.34863304 Cys64;

Query Match: 92.8%; Score 3387; DB 13; Length 751;
Best Local Similarity 96.9%; Pred. No. 4,9e-196;
Matches 654; Conservative 18; Mismatches 21; Indels 60; Gaps 4;

QY 1 MLPGLALLLAAWTARALVPTGNGAGLLAEPCIAHFGRLNHHNVGSKWDSFGSK 60
Db 1 MLPGLALLLAAWTARALVPTGNGAGLLAEPCIAHFGRLNHHNVGSKWDSFGSK 60
QY 61 TCIDTREGILQYCOEYVPELQITNVYEAQPTIQWCKRGKQCKTHPHFV:PYRCLVG 120
Db 61 TCIDTREGILQYCOEYVPELQITNVYEAQPTIQWCKRGKQCKTHPHFV:PYRCLVG 120

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QY 121 EFVSALLVPDKCKLHQRMDVCEBHLHWHITVAKETSEKSTNLHDYGMILPGCIDKFR 180
Db 121 EFVSALLVPDKCKLHQRMDVCEBHLHWHITVAKETSEKSTNLHDYGMILPGCIDKFR 180
QY 181 GYFVCCCLPAESDNDVSDAADAEDSDVWGSADTDYAGSGEDKVE--VAEEBEVAEVE 238
Db 181 GYFVCCCLPAESDNDVSDAADAEDSDVWGSADTDYAGSGEDKVE--VAEEBEVAEVE 238
QY 239 EBEAEDEDEDDGDFVEEAEPEYBEATERTSIAITTTTTTSEVEEVR----- 288
Db 241 DEADDD--DODGDEL-EETSEYEAEERTTSIAITTTTTTSEVEEVRSEQAETG 298
QY 289 -----VPTTAATPDVADK 302
Db 299 PCRAMLSRWYFVAEGKCAPFFYGGCGGNRNFDSEYCMVCGSVLPTTAATPDVADK 358
QY 303 YLETPGDENEHAHFOKAKERLEAKHREMSQVYRWEAEAEQAKNLPKADKAVIQHFE 362
Db 359 YLETPGDENEHAHFOKAKERLEAKHREMSQVYRWEAEAEQAKNLPKADKAVIQHFE 418
QY 363 KYESLEQEAANERQQLVETHMARVEAMLNDRKRLAENYITALQAVPPRPHVFNMLKKY 422
Db 419 KYESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITATQTVPPRPHVFNMLKKY 478
QY 423 VRAEQKDKROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPAVE 482
Db 479 VRAEQKDKROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPAVE 538
QY 483 IQDEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTIVVELLPVNGEFLSD 542
Db 539 IQDEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTIVVELLPVNGEFLSD 598
QY 543 LQPHWFGADSVNPANTENEVEPVDARPAADRGHTIRPGSGLINIKTEISEVKMDAEPH 602
Db 599 LQPHWFGADSVNPANTENEVEPVDARPAADRGHTIRPGSGLINIKTEISEVKMDAEPH 658
QY 603 DSGYEVHHQKLVFFAEIDVGSNGKAIIGLMVGQVVIATVITLVNMLKKQYTSIHGVE 662
Db 659 DSGYEVHHQKLVFFAEIDVGSNGKAIIGLMVGQVVIATVITLVNMLKKQYTSIHGVE 718
QY 663 VDAANTPEERHLSKMQONGYENPTYKFFEQMGN 695
Db 719 VDAANTPEERHLSKMQONGYENPTYKFFEQMGN 751

RESULT 6
Q98SGO
ID Q98SGO PRELIMINARY: PRT: 693 AA.
AC Q98SGO:
DI 01-JUN-2001 (T-EMBLrel. 17, Created)
DI 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DI 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein A.
OS APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hark W.H.:
RJ Thesis (2001), Department of Biological Sciences,
RJ University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1;
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.

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Q91963
ID O91963 PRELIMINARY: PRT: 747 AA.
AC Q91963;
DT 01-NOV-1996 (TRENBLrel. 01, Created);
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update);
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidinae;
OC Xenopodidae.
OX NCBI_taxid=8353;
RN [1];
RS SEQUENCE FROM N.A.
RX MEDLINE=93129227; PubMed=1232805;
RA Okada H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression";
RL Blochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL: S52417; AAB24853.1;
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
DR KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 85.0%; Score 3103; DB 13; Length 747;
Best Local Similarity 81.0%; Pred. No. 6.4e-179;
Matches 598; Conservative 35; Mismatches 41; Indels 54; Gaps 5;

Qy 17 ALEVPDGNAGLLAEPOIAFM-CGRNLMHMYVQNGKWDSPSGTKICIDTREGILQYQOE 75
Db 15 ALEVLVDGNGLLAEPOIAFMSVARLNMHMYVQNGKWDVSS-CIGTKESGILQYQOE 7;

Qy 76 VYPELOITNVYVQNTVQNKCKRCKOCTHPIHFVPIYRCLVGEFVSDALLVPDKCKP 135
Db 72 VYPELOITNVYVQNTVQNKCKRCKOCTHPIHFVPIYRCLVGEFVSDALLVPDKCKP 131

Qy 136 LHQERMDVCETHLHWHTVAKETCEKSTN:HDYGMCLPGCIDKFRGVFVCGCP-AFESDN 195
Db 132 LHQERMDVCETHLHWHTVAKETCEKSTN:HDYGMCLPGCIDKFRGVFVCGCP-AFESDN 191

Qy 196 VDSADAEEDSDVWVGAGTADYADGSEKVFVA-EEEVAAVEEESAEADDECEKGE 253
Db 192 FDSADAEEDSDVWVGAGTADYADGSEKVFVA-EEEVAAVEEESAEADDECEKGE 249

Qy 254 VESEAEPEYEATERTSTATTITTESVEEVVR----- 286
Db 250 ABEPEPEYEATERTSTATTITTESVEEVRCVCEQAETGFCRAK:SRWYDYDYE 309

Qy 289 -----VPTTAASTFDVADKYLETIPGPNFAPPO 317
Db 310 SKCAQFIYGGCGNRNFDSDYCMVCGSV:PAATASTPDADVXLEPN:ENEDREF: 369

Qy 318 KAKERJEAKRERMSQVNRWESEARQAKNLPRADKKAVIQHFQEKVESLEVEANERQ 377
Db 370 KAKERJEAKRERMSQVNRWESEARQAKNLPRADKKAVIQHFQEKVESLEVEANERQ 374

Qy 378 LVETHMARVEAMINDRRRIALENYITALQADPPRRPHVFNMLKKYVRAEQKDRQHTLKH 437
Db 376 LVETHMARVEAMINDRRRIALENYITALQADPPRRPHVFNMLKKYVRAEQKDRQHTLKH 434
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DQ 125 VPRCLVGEFVSALLVPCKCKFLHREKMDCTCHSHLYWLVAKETGCKIMNLDYGMILL 164
QY 173 PCGIDKFRGVEFYCCPIAFESDNVDSADAEEDSDNYWGGADTDYADGSEDKVVEVAEE 232
DB 185 PCGIDEFRGVEFYCCPIEPENDKIDS-DMDEEDSDYWVGDDADYADGG-DKTV-...-E 238
QY 233 EVAVEEEEDDDEDEDEDEVEVEE-ABEYPBEATERIT-SIATITTTTTTIEVEEVVVP 291
DB 239 KPIEEEEEDESIDDEDDDDLDEVEEDYEDYEDYEDYEDYEDYEDYEDYEDYEDYED 295
QY 292 TAASITDAVDKYLETSGDENEHAFKAKERLEAKHRERMSQVMEWEAEARQAKNPKA 351
DB 296 TAASITDAVDKYLETSGDENEHAFKAKERLEAKHRERMSQVMEWEAEARQAKNPKA 355
QY 352 DKXAVIOHFQKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPK 411
DB 356 DKXAVIOHFQKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPK 415
QY 412 PRHVFNMKKYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLVYIERMNSLS 471
DB 416 PRHVLNALKKYSRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLVYIERMNSLS 475
QY 472 LLYNVPAAVEFIQDEVDLQKQNYSDVLANMISEPRISYGNDAIMPSTETKTIVEL 531
DB 476 LLYKVPAAVEFIQDEVDLQKQNYSDVLANMISEPRISYGNDAIMPSTETKTIVEL 535
QY 532 LPVNGFSLDDLPWHSFGADSVDPANTENEVEPVDARPAADRGITTPRSGSLINKTES 591
DB 536 LPDNGFSLDDLPWHSFGADSVDPANTENEVEPVDARPAADRGITTPRSGSLINKTES 595
QY 592 SEVKMDAEFRHDSGYEYHOKLVFFAEEDVGSNGKAIIGLVGGVVIATVITVLVMIKK 651
DB 596 AELKMEFQDSDGYEYHOKLVFFAEEDVGSNGKAIIGLVGGVVIATVITVLVMIKK 655
QY 652 QYTIHGGVVEVDAATFEERHLSKMOONGYENPTYKFFEQMKN 695
DB 656 QYTIHGGVVEVDAATFEERHLSKMOONGYENPTYKFFEQMKN 699

RESULT 10
Q9PVL1 PRELIMINARY: PRT: 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Palica K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor superegene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2003).
DR EMBL: AF030341; AAF12698.1; .
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA: 64753 MW: 3ABBB851863A19D CKC64;

Query Match 75.8%; Score 2767.5; DB 13; Length 569;

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Best Local Similarity 93.5%; Pred. No. 7.6e-159;
Matches 535; Conservative 14; Mismatches 18; Indels 5; Gaps 4;
QY 126 ALLVPDKCKFLHREKMDCTCHSHLYWLVAKETGCKIMNLDYGMILLPCGIDKFRGVEFY 185
DB 1 ALLVPDKCKFLHREKMDCTCHSHLYWLVAKETGCKIMNLDYGMILLPCGIDKFRGVEFY 60
QY 186 CCPLAEESDNVDSADAEEDSDNYWGGADTDYADGSEDKVVE--VAEEVEEVAEEVEEAD 243
DB 61 CCPLAEESDNVDSADAEEDSDNYWGGADTDYADGSEDKVVEEQPEDEELTVVEDEAD 120
QY 244 DDEDDGDEVEVEEAEFEYERATERTTSIATITTTTTTIEVEEVVVPITAASTDVADKY 303
DB 121 DD-DDDDGDEL-EETEEYEEATERITTSIATITTTTTTIEVEEVVVPITAASTDVADKY 178
QY 304 LETPGDENEHAFKAKERLEAKHRERMSQVMEWEAEARQAKNPKADKKAVIOHFQK 363
DB 179 LETPGDENEHAFKAKERLEAKHRERMSQVMEWEAEARQAKNPKADKKAVIOHFQK 238
QY 364 VESLEGEAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPRHRHVFNMKKYV 423
DB 239 VESLEGEAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPRHRHVFNMKKYV 298
QY 424 RAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLVYIERMNSLSLLYNVPAVAEEI 483
DB 299 RAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLVYIERMNSLSFLYNVPAVAEEI 358
QY 484 QDEVDRLQKQNYSDVLANMISEPRISYGNDAIMPSTETKTIVELLVNGFSLDDL 543
DB 359 QDEVDRLQKQNYSDVLANMISEPRISYGNDAIMPSTETKTIVELLVNGFSLDDL 418
QY 544 QPWHFSGADSVDPANTENEVEPVDARPAADRGITTPRSGSLINKTEEISEVKMDAEFRHD 603
DB 419 QPWHFSGADSVDPANTENEVEPVDARPAADRGITTPRSGSLINKTEEISEVKMDAEFRHD 478
QY 604 SGYEYHOKLVFFAEEDVGSNGKAIIGLVGGVVIATVITVLVMIKKQYTSIHHGVVEV 663
DB 479 SGYEYHOKLVFFAEEDVGSNGKAIIGLVGGVVIATVITVLVMIKKQYTSIHHGVVEV 538
QY 664 DAATVTEERHLSKMOONGYENPTYKFFEQMKN 695
DB 539 DAATVTEERHLSKMOONGYENPTYKFFEQMKN 569

RESULT 1:
Q99K32 PRELIMINARY: PRT: 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 58.4 kDa protein (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005490; AAH05490.1; .
DR HSSP: P05067; IAAP.
DR MGD: MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.

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DR SMART: SMO03131; KU: 1.
DR PROSITE: PS00319; A4_EXTRA: 1.
DR PROSITE: PS00320; A4_INTRA: 1.
DR PROSITE: PS00280; BPT_KN172_1: 1.
DR PROSITE: PS00279; BPT_KN172_2: 1.
KW Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA: 68391 MW: 68022;4C9A7D172 CRC64:
      72.2%; Score 2635.5; DB 11; Length 637;
Query Match
Best Local Similarity 85.7%; Pred. No. 7 5e-152;
Matches 520; Conservative 4; Mismatches 8; Indels 75; Gaps 1;
QY 164 NLHDYGMLLPCGIDKFRGVFVCCPLAESDVSADAEEDSDVMWGADTDVADGSED 223
DB 1 NLHDYGMLLPCGIDKFRGVFVCCPLAESDVSADAEEDSDVMWGADTDVADGSED 60
QY 224 KYVEVAEEVAEVEEEDDDDDGDEVEEAEPEVEEATERTISTATITTTTIESV 283
DB 61 KYVEVAEEVAEVEEEDDDDDGDEVEEAEPEVEEATERTISTATITTTTIESV 120
QY 284 EYVVR----- 288
DB 121 EYVVRVCSQAETGPERAMISRWYFDVTEGKCVDFYCGGSGNKNNEDETEYCVAGVGS 190
QY 289 -----VPTAASTPDVDKYLETTPGDENEHAHFQKAKERLEAKHP 328
DB 181 VSTGSLTKTSEPLDQPKLPTTAASTPDVDKYLETTPGDENEHAHFQKAKERLEAKHR 240
QY 329 ERMSQVREWEAEERQAKNLPRADKAVTQHFEKVESLEQEAANEERQOLVETHMARVEA 386
DB 241 ERMSQVREWEAEERQAKNLPRADKAVTQHFEKVESLEQEAANEERQOLVETHMARVEA 300
QY 389 MLNDRESIALENVITLQAVPRPRHVFNNLKKYVRAEQKDRQHTLKHFPHVHMVDPKKA 449
DB 301 MLNDRRRLALENTLQAVPRPRHVFNNLKKYVRAEQKDRQHTLKHFPHVHMVDPKKA 360
QY 449 AQIRSQVMTLRLVYIERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISE 508
DB 361 AQIRSQVMTLRLVYIERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISE 420
QY 509 PRISYGNDAIMPSTETKTTVELLPVNGEFLDQPHSFGADSVPAANTEVEFVDAR 568
DB 421 PRISYGNDAIMPSTETKTTVELLPVNGEFLDQPHSFGADSVPAANTEVEFVDAR 480
QY 569 PAADRGLTTPGSLGNKITERISEVKMDAEFRHDSGYEVHHQKLVFFAEVGSNKGAI 628
DB 481 PAADRGLTTPGSLGNKITERISEVKMDAEFRHDSGYEVHHQKLVFFAEVGSNKGAI 540
QY 629 GLMVGGVVIAVTIVTLVLMKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYK 688
DB 541 GLMVGGVVIAVTIVTLVLMKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYK 600
QY 689 FFEQMOM 695
DB 601 FFEQMOM 607
RESULT 12
O93296 PRELIMINARY; PRI: 534 AA.
AC O93296
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
OS Amyloid protein (Fragment).
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
R "Increased production of amyloid precursor protein provides a
R substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EXRL; AF042098; AAC25052.1; -.
DR HSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03454; Beta-APP; 1.
DR PRINTS; PR00203; AMYJOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA: 60597 MW: FB53ECC2E6604C92 CRC64:
      71.6%; Score 2613; DB 13; Length 534;
Query Match
Best Local Similarity 94.8%; Pred. No. 1.4e-149;
Matches 506; Conservative 13; Mismatches 11; Indels 4; Gaps 3;
QY 164 NLHDYGMLLPCGIDKFRGVFVCCPLAESDVSADAEEDSDVMWGADTDVADGSED 223
DB 3 NLHDYGMLLPCGIDKFRGVFVCCPLAESDVSADAEEDSDVMWGADTDVADGSED 62
QY 224 KYVEVAEVAEVEEEDDDDDGDEVEEAEPEVEEATERTISTATITTTTITE 281
DB 63 KYVEEOPDEDELTVVEDECDADD-DDDDGDGI-EETEEVEEATERTISTATITTTITE 120
QY 282 SVSEVYRVPTTAASTPDVDKYLETTPGDENEHAHFQKAKERLEAKHRKMSQVREWEA 341
DB 121 SVSEVYRVPTTAASTPDVDKYLETTPGDENEHAHFQKAKERLEAKHRKMSQVREWEA 180
QY 342 ERQAKNLPRADKAVTQHFEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENY 401
DB 181 ERQAKNLPRADKAVTQHFEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENY 240
QY 402 ITALQAVPRPRHVFNNLKKYVRAEQKDRQHTLKHFPHVHMVDPKKAQIRSQVMTLRLV 461
DB 241 ITALQAVPRPRHVFNNLKKYVRAEQKDRQHTLKHFPHVHMVDPKKAQIRSQVMTLRLV 300
QY 462 IYERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMP 521
DB 301 IYERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMP 360
QY 522 LTETKTTVELLPVNGEFLDQPHSFGADSVPAANTEVEFVDARPAADRGLTTRPGS 581
DB 361 LTETKTTVELLPVNGEFLDQPHSFGADSVPAANTEVEFVDARPAADRGLTTRPGS 420
QY 582 GLTNKITEISVKMDAEFRHDSGYEVHHQKLVFFAEVGSNKGAIIGLMVGGVVIAVTI 641
DB 421 GLTNKITEISVKMDAEFRHDSGYEVHHQKLVFFAEVGSNKGAIIGLMVGGVVIAVTI 480
QY 642 VITLVMKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMOM 695
DB 481 VITLVMKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMOM 534
RESULT 13
O73683 PRELIMINARY; PRI: 780 AA.
AC O73683
DI 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
OS Alzheimer's disease amyloid A4 protein homolog precursor {Contains:
OS beta-amyloid protein (Beta-APP) (A-beta)}.
ON APP.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.
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 19: /SIDSL/qcgdata/geneseq/geneseq-cmb1/AA1998.DAT:*
 20: /SIDSL/qcgdata/geneseq/geneseq-cmb1/AA1999.DAT:*
 21: /SIDSL/qcgdata/geneseq/geneseq-cmb1/AA2000.DAT:*
 22: /SIDSL/qcgdata/geneseq/geneseq-cmb1/AA2001.DAT:*
 23: /SIDSL/qcgdata/geneseq/geneseq-cmb1/AA2002.DAT:*
 24: /SIDSL/qcgdata/geneseq/geneseq-cmb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3651	100.0	697	21	Human APPSW-KK am
2	3651	100.0	697	22	Human amyloid prot
3	3651	100.0	697	22	Human amyloid prec
4	3651	100.0	697	22	Human amyloid prec
5	3651	100.0	697	22	Human amyloid prec
6	3651	100.0	697	22	Human amyloid prec
7	3651	100.0	697	23	Human APP695-SW-KK
8	3643	99.8	697	21	Human APP695-KK am
9	3643	99.8	697	22	Human amyloid prot

10	3643	99.8	697	22	AAE06865	Human amyloid prec
11	3643	99.8	697	22	AAU06609	Human amyloid prec
12	3643	99.8	697	22	AAU07208	Human beta-amyloid
13	3643	99.8	697	22	AAE02587	Human amyloid prec
14	3643	99.8	697	23	ABB78596	Human APP695-KK pr
15	3641	99.7	695	21	AAV88435	Human APP695-SW va
16	3641	99.7	695	22	AAE10633	Human amyloid prot
17	3641	99.7	695	22	AAE06863	Human amyloid prec
18	3641	99.7	695	22	AAU06607	Human amyloid prec
19	3641	99.7	695	22	AAU07206	Human beta-amyloid
20	3641	99.7	695	22	AAE02585	Human amyloid prec
21	3641	99.7	695	23	ABB78594	Human APP695-SW pr
22	3638	99.6	697	21	AAV88430	Human APP695-VF-KK
23	3638	99.6	697	22	AAE10637	Human amyloid prot
24	3638	99.6	697	22	AAE06867	Human amyloid prec
25	3638	99.6	697	22	AAU06611	Human amyloid prec
26	3638	99.6	697	22	AAU07210	Human beta-amyloid
27	3638	99.6	697	22	AAE02589	Human amyloid prec
28	3638	99.6	697	23	ABB78598	Human APP695-VF-KK
29	3636	99.6	695	18	AAW19504	APP695 mutant A-be
30	3636	99.6	695	18	AAW19490	Sequence of human
31	3633	99.5	695	9	APR1692	APP695. Homo sapi
32	3633	99.5	695	13	AAE26338	Human beta-amyloid
33	3633	99.5	695	19	AAV20233	Amyloid precursor
34	3633	99.5	695	20	AAV07221	Human APP695 amino
35	3633	99.5	695	21	AAV88434	Human beta amyloid
36	3633	99.5	695	21	AAV44705	Human wild-type am
37	3633	99.5	695	22	AAE10632	Human wild-type am
38	3633	99.5	695	22	AAE06862	Human amyloid prec
39	3633	99.5	695	22	AAU06606	Human amyloid prec
40	3633	99.5	695	22	AAE02584	Human amyloid prec
41	3633	99.5	695	23	ABG32723	Human APP695 prote
42	3633	99.5	695	23	ABB78593	Human amyloid prec
43	3633	99.5	695	23	AAAG68315	Amino acid sequenc
44	3633	99.5	695	24	ABB9604	Human beta amyloid
45	3630	99.4	695	20	AAV49690	

ALIGNMENTS

RESULT 1
 AAY88429
 ID AAY88429 standard; Protein: 697 AA.
 AC AAY88429;
 C: 03-AUG-2000 (first entry)
 DE Human APPSW-KK amino acid sequence.
 XX
 XX Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
 KW Alzheimer's disease; beta secretase site; APPSW-KK.
 XX
 XX Homo sapiens.
 XX
 XX WO200017369-A2.
 XX
 XX 30-MAR-2000.
 XX
 XX 23-SEP-1999; 99WO-US20881.
 XX
 XX 24-SEP-1998; 98US-0101594.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yar R;
 PI WPI: 2000-303209/26.
 DR N-PSDB; AAA15666.
 DR
 XX New enzyme designated human aspartase useful in research into
 PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

the beta secretase site to produce amyloid beta peptide -
Claim 133; Page 143-147; 183pp; English.

This sequence represents a modified version of the human amyloid precursor protein (APP) amino acid sequence. The sequence is used in an example of the method of the invention, to show that modification of APP increases beta amyloid protein processing. The invention relates to a protease (e.g. Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DTG or DTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.

Query Match 100.0%; Score 3651; DB 21; Length 697;
Best Local Similarity 100.0%; Pred. No. 1,40-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAFQIAMFCGRINMNMNVONGKWSDFSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAFQIAMFCGRINMNMNVONGKWSDFSGTK 60
QY 61 TCIDTKEGILQCOEYVPELQITNVVEANQVTONKCKRGKCKTSPHEVPIRCLVG 120
DB 61 TCIDTKEGILQCOEYVPELQITNVVEANQVTONKCKRGKCKTSPHEVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVVCETHLHWHVAKETCSKSTNLHDYGMILPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVVCETHLHWHVAKETCSKSTNLHDYGMILPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWNGCADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWNGCADTDYADGSEDKVVEAEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTITSEVEEVVRVPTAASIPFAY 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTITSEVEEVVRVPTAASIPFAY 300
QY 301 DKYLETPGDENHAFQAKERLEAKHREMSQVNRKEAEFRQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENHAFQAKERLEAKHREMSQVNRKEAEFRQAKNLPKADKAVIQHF 360
QY 361 QKVESLEQEAANERCOLVETHMARVEAMLDNRRLALENTTALQAVPPRPHVFNKJK 420
DB 361 QKVESLEQEAANERCOLVETHMARVEAMLDNRRLALENTTALQAVPPRPHVFNKJK 420
QY 421 KYVRAEQDKRQTHLKHFEVRVMDPKAAQIRSQVNTHLRVYERKNOSLSLLNVPAVA 480
DB 421 KYVRAEQDKRQTHLKHFEVRVMDPKAAQIRSQVNTHLRVYERKNOSLSLLNVPAVA 480
QY 481 EETQDEVDLLOKQNYSDQVLANMISPRISYKNDALMPSLITEKITVELLPNGEFL 540
DB 481 EELQDEVDLLOKQNYSDQVLANMISPRISYKNDALMPSLITEKITVELLPNGEFL 540
QY 541 DDLQPHSFGADSVANTENVEPVDARPAADRGITTRPGSGELNKTKEEISEVNLDAEP 600
DB 541 DDLQPHSFGADSVANTENVEPVDARPAADRGITTRPGSGELNKTKEEISEVNLDAEP 600
QY 601 RHDGSEVVEHQKLVFAEDVGSNGKGAITGLMVGGVVIATVITLVMKKQYTSIHGV 660
DB 601 RHDGSEVVEHQKLVFAEDVGSNGKGAITGLMVGGVVIATVITLVMKKQYTSIHGV 660

QY 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMKNK 697
PS |||||
XX |||||
DB 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMKNK 697
AAE10536
AAE10536 standard; Protein: 697 AA.
AAE10536:
10-DEC-2001 (first entry)
Human amyloid protein precursor 695-Sw-KK (APP695-Sw-KK) isoform.
Human; aspartyl protease 1; Aspl; amyloid precursor protein;
Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
amyloid plaque; neuronal loss; proteolytic; neuroprotective;
APP695-Sw-KK; mutant; muten.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
FT Misc-difference 595 /note= "Wild-type Lys substituted with Asn"
ET Misc-difference 596 /note= "Wild-type Met substituted with Leu"
XX GB2357767-A.
XX 04-JUL-2001.
XX 22-SEP-2000; 2000GB-0023315.
XX 23-SEP-1999; 99US-0155493.
XX 23-SEP-1999; 99US-0404133.
XX 23-SEP-1999; 99MO-US20881.
XX 13-OCT-1999; 99US-0416901.
XX 06-DEC-1999; 99US-0169232.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX Bieskowksi MJ, Gurney M;
WP1: 2001-44208/48.
XX N-PSDB; AAD17872.
XX Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX Example 6; Page 117-119; 187pp; English.
XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
XX Aspl proteins which lack transmembrane domain or amino terminal
XX domain or cytoplasmic domain and retains alpha-secretase activity
XX and amyloid protein precursor (APP) processing activity. The proteins
XX of the invention are useful for assaying hu-Aspl alpha-secretase
XX activity, which in turn is useful for identifying modulators of
XX hu-Aspl alpha-secretase activity, where modulators that increase
XX hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
XX disease (AD) which causes progressive dementia with consequent
XX formation of amyloid plaques, neurofibrillary tangles, gliosis and
XX neuronal loss. Hu-Aspl protease substrate is useful for assaying
XX hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
XX the substrate under acidic conditions and determining the level of
XX hu-Aspl proteolytic activity. The present sequence is human amyloid
XX protein precursor 695-Sw-KK (APP695-Sw-KK) isoform which is obtained
XX by the addition of two lysine residues (KK motif) at the C-terminal
XX of App695-Sw isoform which is generated by the Swedish mutation
XX APP695, where Lys at position 595 is replaced with Asn and Met at

CC position 595 is replaced with Leu. APP695-Sw-KK isoform is useful
for assaying the beta-secretase activity of human aspartyl protease
2a (Hu-Asp2a) protein.

XX	Sequence	697 AA:
XX	Query Match	100.0%; Score 3651; DB 22; Length 697;
XX	Best Local Similarity	100.0%; Pred. No. 1.4e-256;
XX	Matches 697;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MLPGLALLLAATARAALVPTDGNAGLLAEPOIAFMCGRLNMHNVMQNGKWDSPSGTK 60
DB	1	MLPGLALLLAATARAALVPTDGNAGLLAEPOIAFMCGRLNMHNVMQNGKWDSPSGTK 60
QY	61	TCIDTKEGILQCYEYVPELQITNNVEANQPVTIONWCKGRKQCKTHPHFVTPYRC:VG 120
DB	61	TCIDTKEGILQCYEYVPELQITNNVEANQPVTIONWCKGRKQCKTHPHFVTPYRC:VG 120
QY	121	EFVSDALLVPDKCFELHQRMDVCEITHLHWHTVAKETCEKSTNLRDYGMLLPCGIDKFR 180
DB	121	EFVSDALLVPDKCFELHQRMDVCEITHLHWHTVAKETCEKSTNLRDYGMLLPCGIDKFR 180
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKYVEVAEEFEVVEE 240
DB	181	GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKYVEVAEEFEVVEE 240
QY	241	EADDDEDDEGDEVEEAEPEEAEATERTTSTIAITTTTTIESVEVVRVP:TAASIPDAV 300
DB	241	EADDDEDDEGDEVEEAEPEEAEATERTTSTIAITTTTTIESVEVVRVP:TAASIPDAV 300
QY	301	DAYLETDPDENEFAHFQAKERLEAKHRMSQVNRWEPKAKNLPKAPKAVI:CHF 360
DB	301	DAYLETDPDENEFAHFQAKERLEAKHRMSQVNRWEPKAKNLPKAPKAVI:CHF 360
QY	361	QEKVESLEQEAANERQQLVETIHARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB	361	QEKVESLEQEAANERQQLVETIHARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY	421	KYVRAEQDKROHTLKHFEHVRVVDPKAAQIRSQVMTILRV:YERMGSLSLLYNPPAVA 480
DB	421	KYVRAEQDKROHTLKHFEHVRVVDPKAAQIRSQVMTILRV:YERMGSLSLLYNPPAVA 480
QY	481	BEIQDEVDDELLOKEQNSDDVLANNISPRISYGNDAKLPSTLTKTVELLPVNGE:SL 540
DB	481	BEIQDEVDDELLOKEQNSDDVLANNISPRISYGNDAKLPSTLTKTVELLPVNGE:SL 540
QY	541	DDLQPHWSEFGADSVANTENEPVDPADPAADRGTLTPGSGLTNKTKEESSEVNLDAFF 600
DB	541	DDLQPHWSEFGADSVANTENEPVDPADPAADRGTLTPGSGLTNKTKEESSEVNLDAFF 600
QY	601	RHDSGYEVHHQKLVFEAEVDGSKGAIGLWGVGVVIA:VITLVMKKGYTSIHGV 660
DB	601	RHDSGYEVHHQKLVFEAEVDGSKGAIGLWGVGVVIA:VITLVMKKGYTSIHGV 660
QY	661	VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMNKK 697
DB	661	VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMNKK 697

RESULT 3
AAE06866
ID AAE06866 standard; Protein: 697 AA.

XX AC AAE06866;

XX DT 23-OCT-2001 (first entry)

XX DE Human amyloid precursor protein 695-Sw-KK (APP695-Sw-KK) isoform.

XX KW Human: aspartyl protease; Asp; beta-amyloid precursor protein 695-Sw-KK;
beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nontropic;
neuroprotective; antisense therapy; gene therapy; APP695-Sw-KK; mutant;

KW	muteln.
XX	
OS	Homo sapiens.
OS	Synthetic.
PH	Key Location/Qualifiers
FT	Misc-difference 595
FT	/note= "Wild type Lys substituted with Asn"
FT	Misc-difference 596
FT	/note= "Wild type Met substituted with Leu"
XX	WO200150829-A2.
XX	19-JUL-2001.
XX	09-MAY-2001; 2001WO-IB00799.
XX	09-MAY-2001; 2001WO-IB00799.
XX	(BIEN/) BIENKOWSKI M J.
XX	(GURN/) GURNEY M E.
XX	(HEIN/) HEINRIKSON R L.
XX	(PARO/) PARODI L A.
XX	(YANK/) YAN R.
XX	Fienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX	WPI; 2001-483072/52.
XX	N-PSDB; AAD13028.
XX	Novel purified polypeptide comprising fragment of mammalian aspartyl
XX	protease 2, lacking Asp2 transmembrane domain and retaining beta
XX	secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX	activity
XX	Example 6; Page 147-149; 185pp; English.

The invention relates to human aspartyl proteases (Hu-Asp). beta-amyloid precursor protein (APP) isoforms and their corresponding DNA molecules. Human aspartyl proteases can act as beta-secretase proteases useful for treating Alzheimer's disease. APP isoforms are useful for identifying modulators of amyloid-beta peptide production, for use in designing therapeutics for the treatment and prevention of Alzheimer's disease, and neuronal loss. APP isoforms are also used in methods for identifying inhibitors and modulators of human Asp2 activity. The invention relates to a method for identifying agents that modulate the activity of human aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used as a means to screen in cellular assays for the inhibitors of beta- and gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in polymerase chain reactions (PCR). The probes are useful for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and Southern blots. The present sequence is modified human amyloid precursor protein 695-Swedish (APP695-Sw-KK) isoform. APP695-Sw-KK isoform is obtained by addition of two Lys residues (KK motif) at the C-terminal end of APP695-Sw isoform. APP695-Sw isoform is obtained by Swedish KM-NL mutation in APP695 isoform, where Lys at position 595 is replaced with Asn. Met at position 596 is replaced with Leu. APP695-Sw-KK isoform is useful for assaying the beta-secretase activity of human aspartyl protease 2a (Hu-Asp2a) protein.

XX Sequence 697 AA;

XX Query Match 100.0%; Score 3651; DB 22; Length 697;

XX Best Local Similarity 100.0%; Pred. No. 1.4e-256;

XX Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATARAALVPTDGNAGLLAEPOIAFMCGRLNMHNVMQNGKWDSPSGTK 60

DB 1 MLPGLALLLAATARAALVPTDGNAGLLAEPOIAFMCGRLNMHNVMQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQCYEYVPELQITNNVEANQPVTIONWCKGRKQCKTHPHFVTPYRC:VG 120

Db	61	TCIDTKSGILQYQGEVPELPDGLITVYVGNQPVITQNNCKSGKQCKTHIEFVLYPNCLVGE	122
Qy	121	EFVSDAILVDPCKFLHQRMDVCEIHLRHITVAKETCSFKSNLKYCKMLPGCDKPF	160
Db	121	EFVSDAILVDPCKFLHQRMDVCEIHLRHITVAKETCSFKSNLKYCKMLPGCDKPF	160
Qy	181	GVEFYCCPLAESUNVSADAEESDDSVWVGGAUDYADGSDKVVVEAEAEFEVAEVE	240
Db	181	GVEFYCCPLAESUNVSADAEESDDSVWVGGAUDYADGSDKVVVEAEAEFEVAEVE	240
Qy	241	EADDDDEDDGDEVEEEAEPEEATERTTSATTTITTTESVEEVVVFVTTAASTPDV	300
Db	241	EADDDDEDDGDEVEEEAEPEEATERTTSATTTITTTESVEEVVVFVTTAASTPDV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEACAKNLPAKPKKAVIOHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEACAKNLPAKPKKAVIOHF	360
Qy	361	QEKVESLQEAANPEHQGLVEITHMARVEAMLNDRRLALENYITALQAVGPRFHHVFNMLK	420
Db	361	QEKVESLQEAANPEHQGLVEITHMARVEAMLNDRRLALENYITALQAVGPRFHHVFNMLK	420
Qy	421	KYVRAEQKDRQHTLKHPEHVRMVDPKKAAQIRSQVMHLRVIVYERMNQSLSLYNNPVA	480
Db	421	KYVRAEQKDRQHTLKHPEHVRMVDPKKAAQIRSQVMHLRVIVYERMNQSLSLYNNPVA	480
Qy	481	BEIODEVDELLOKEQNSDDVLANWISPEPRISYCNDAHMLSTETKTITVELLPVNGEFS	540
Db	481	BEIODEVDELLOKEQNSDDVLANWISPEPRISYCNDAHMLSTETKTITVELLPVNGEFS	540
Qy	541	DDLQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETISEVNLDADF	600
Db	541	DDLQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETISEVNLDADF	600
Qy	601	RHDSGYEVHHOKLVFFAEVGSNGKAIIGLMVGQVVIATVIVITLVMKKKQVSTIHGV	660
Db	601	RHDSGYEVHHOKLVFFAEVGSNGKAIIGLMVGQVVIATVIVITLVMKKKQVSTIHGV	660
Qy	661	VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK	697
Db	661	VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK	697
RESULT	4		
AAU06610			
ID	AAU06610	standard; Protein: 697 AA.	
AC	AAU06610;		
CC			
CT	24-OCT-2001	(first entry)	
DE		Human Amyloid precursor protein mutant, APP695-SW-KK.	
DE			
KW		Human; Aspartyl protease; Asp2b; beta-secretase; ectotropic;	
KW		neuroprotective; amyloid protein precursor; App; Alzheimer's disease;	
KW		amyloid-beta; Abeta; APP695-SW-KK; mutant; mutant.	
XX			
CS		Homo sapiens.	
XX			
FT		Location/Qualifiers	
FT		Misc-difference 595..596	
FT		/note= "Wild-type Lys-Met substituted by Asn-Leu"	
FT		Misc-difference 696..697	
FT		/note= "2 Extra Lys residues added compared to	
FT		wild-type APP695"	
XX			
PN		WO200149098-A2.	
XX			
PD		12-JUL-2001.	
XX			
PF		09-MAY-2001; 2001WO-IB00798.	
XX			
PR		09-MAY-2001; 2001WO-IB00798.	

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360

 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360

 QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHEVFNMLK 420

 DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHEVFNMLK 420

 QY 421 KYVRAEQDKROHTLKHFEHVMVDPKKAQAQIRSQVMTHLRVYIERMNSLSLLYNPAPA 480

 DB 421 KYVRAEQDKROHTLKHFEHVMVDPKKAQAQIRSQVMTHLRVYIERMNSLSLLYNPAPA 480

 QY 481 EEIQDEYDELLQKQNYSDOVLANNMISEPRISYGNDAIMPSTETTKITVELLPNGEFSL 540

 DB 481 EEIQDEYDELLQKQNYSDOVLANNMISEPRISYGNDAIMPSTETTKITVELLPNGEFSL 540

 QY 541 DDLOPHWSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNIKTEISEVNLDAEF 600

 DB 541 DDLOPHWSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNIKTERISEVNLDAEF 600

 QY 601 RHDGSEYVHHOKLVFFAEIDVGSNGKAIIGLVGGVWATVIVITLVMLKKQYTSIHGV 660

 DB 601 RHDGSEYVHHOKLVFFAEIDVGSNGKAIIGLVGGVWATVIVITLVMLKKQYTSIHGV 660

 QY 661 VEVDAAVTPPEERHLSKKQNGYENPTYKFFEQMONKK 697

 DB 661 VEVDAAVTPPEERHLSKKQNGYENPTYKFFEQMONKK 697

RESULT: 5

AAU07209

ID AAU07209 standard; Protein: 697 AA.

XX AAU07209;

24-OCT-2001 (first entry)

Human beta-amyloid protein precursor, APP695-Sw-KK.

Human: aspartyl protease 1; Asp-1; neotropic; neuroprotective;

aspartyl protease 2; Asp2; amyloid protein precursor; APP;

beta-secretase; Alzheimer's disease; APP695-Sw-KK.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 595

FT /note= "Wild type Lys substituted by Asn"

FT Misc-difference 596

FT /note= "Wild type Met substituted by Leu"

FN W0200149097-A2.

XX 12-JUL-2001.

XX 09-MAY-2001: 2001WO-IB00797.

XX 09-MAY-2001: 2001WO-IB00797.

XX (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

XX WPI: 2001-502548/55.

XX N-PSDB; AAS11709.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

PI activity -

XX

XX Example 6; Page 147-149; 185pp; English.

XX The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognizable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP695-Sw-KK,
 CC used in the method of the invention.

XX Sequence 697 AA;

SQ

Query Match 100.0%; Score 3651; DB 22; Length 697;

Best Local Similarity 100.0%; Pred. No. 1.4e-256;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQIAPFCGRNLNMHMNVQNGKWSDSFGTK 60

 DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQIAPFCGRNLNMHMNVQNGKWSDSFGTK 60

 QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONCKRGRKOCKTHPFIPLPYRCLVG 120

 DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONCKRGRKOCKTHPFIPLPYRCLVG 120

 QY 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSEKSNLHDYGMLLPGCIDKFR 180

 DB 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSEKSNLHDYGMLLPGCIDKFR 180

 QY 181 GVFEVCCPLAESDNDVDSADAEDSDVWVGADTDYADGSEDKVVEAEVEAEVEE 240

 DB 181 GVFEVCCPLAESDNDVDSADAEDSDVWVGADTDYADGSEDKVVEAEVEAEVEE 240

 QY 241 EADDEDDGDEVEEAEPEPEATEERTTSIATTTTITTESVEEVVPTTAASIPDAV 300

 DB 241 EADDEDDGDEVEEAEPEPEATEERTTSIATTTTITTESVEEVVPTTAASIPDAV 300

 QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360

 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360

 QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHEVFNMLK 420

 DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHEVFNMLK 420

 QY 421 KYVRAEQDKROHTLKHFEHVMVDPKKAQAQIRSQVMTHLRVYIERMNSLSLLYNPAPA 480

 DB 421 KYVRAEQDKROHTLKHFEHVMVDPKKAQAQIRSQVMTHLRVYIERMNSLSLLYNPAPA 480

 QY 481 EEIQDEYDELLQKQNYSDOVLANNMISEPRISYGNDAIMPSTETTKITVELLPNGEFSL 540

 DB 481 EEIQDEYDELLQKQNYSDOVLANNMISEPRISYGNDAIMPSTETTKITVELLPNGEFSL 540

 QY 541 DDLOPHWSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNIKTEISEVNLDAEF 600

 DB 541 DDLOPHWSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNIKTEISEVNLDAEF 600

QY 501 RHDSGYEVHVKLVFFAEDVGSNGKGLIIGLMVGGVVIATVITVILVLMKKKKQYTSIHRSV 660
 DB 601 RHDSGYEVHVKLVFFAEDVGSNGKGLIIGLMVGGVVIATVITVILVLMKKKKQYTSIHRSV 660
 QY 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697
 DB 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697

RESULT 6
 AAE02588
 ID AAE02588 standard; Protein: 697 AA.
 AC AAE02588;
 XX
 DT 10-AUG-2001 (first entry)
 DE Human amyloid precursor protein 695-Sw-KK (APP695-Sw-KK).
 KW Human; alpha-secretase; amyloid precursor protein 695-Sw-KK; therapy;
 KW APP695-Sw-KK; Alzheimer's disease; anti-Alzheimer's.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W02001:23533 A2.
 XX
 PD C5-APR-2001.
 XX
 PF 22-SEP-2000; 2000NO-US26380.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99NO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-C169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienkowski MJ;
 XX
 WPI: 2001-290516/30.
 DR N-PSNR; AAD05746.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 protein, useful for the treatment of Alzheimer's disease -
 XX
 PS Example 6; Page 146-148; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 secretase site of the amyloid precursor protein (APP) and methods of
 identifying those enzymes. The methods may be used to identify enzymes
 that may be used to cleave the alpha-secretase cleavage site of the APP
 protein. The enzymes may be used to treat or modulate the progress of
 Alzheimer's disease. The present sequence is human APP695-Sw-KK. This
 sequence contains a Sw mutation which is characterised by a K to N.
 CC alteration at positions 595-596 and two lysine residues at the
 CC carboxyl-terminal end.
 XX
 SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 22; Length 697;
 Best Local Similarity 100.0%; Pred. No. 1.4e-256;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPOLAMFCGRLNMHNVQNGKSDSFGTK 60
 DB 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPOLAMFCGRLNMHNVQNGKSDSFGTK 60
 QY 61 TCIDTKGSLIYQCQEVPELQITNVVEANQPVTIQNCKRQCKQTHPHFVTPYRCVCS 120
 DB 61 TCIDTKGSLIYQCQEVPELQITNVVEANQPVTIQNCKRQCKQTHPHFVTPYRCVCS 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSEKSTNLHDYGMLLFCGIDKFR 180

DB 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSEKSTNLHDYGMLLFCGIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEDSDVVMWGADTDYADGSEKVVVEAEVEEVAEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEDSDVVMWGADTDYADGSEKVVVEAEVEEVAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEYEAERTTSIATTTTITESTVEEVVVRPTTAASTPDV 300
 DB 241 EADDDDEDDGDEVEEAEPEYEAERTTSIATTTTITESTVEEVVVRPTTAASTPDV 300
 QY 301 DKYLETGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
 DB 301 DKYLETGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
 QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVNMLK 420
 DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVNMLK 420
 QY 421 KYVRAEQDKRQHTLKHFEHVVMYDPKKAACIRSOVMTHLRVYIYERMNQSLSLLYNPVAV 480
 DB 421 KYVRAEQDKRQHTLKHFEHVVMYDPKKAACIRSOVMTHLRVYIYERMNQSLSLLYNPVAV 480
 QY 481 BEIQDEYDELLQKQNYSDVLANMISEPRISYGNDALMPSLTETKITVELLPVNGEFSL 540
 DB 481 BEIQDEYDELLQKQNYSDVLANMISEPRISYGNDALMPSLTETKITVELLPVNGEFSL 540
 QY 541 DDLOPWHISFGADSVPAANTEVEVVDARPAADRGITTRPGSGLTNKTEELISEVNLDAEF 600
 DB 541 DDLOPWHISFGADSVPAANTEVEVVDARPAADRGITTRPGSGLTNKTEELISEVNLDAEF 600
 QY 601 RHDSGYEVHVKLVFFAEDVGSNGKGLIIGLMVGGVVIATVITVILVLMKKKKQYTSIHRSV 660
 DB 601 RHDSGYEVHVKLVFFAEDVGSNGKGLIIGLMVGGVVIATVITVILVLMKKKKQYTSIHRSV 660
 QY 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697
 DB 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697

RESULT 7
 ABB78597
 ID ABB78597 standard; Protein: 697 AA.
 AC ABB78597;
 XX
 DT 16-JUL-2002 (first entry)
 DE Human APP695-Sw-KK protein sequence SEQ ID NO:18.
 KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
 KW proteolytic; amyloid precursor protein; APP.
 OS Homo sapiens.
 XX
 PN GB2367060-A.
 XX
 PD 27-MAR-2002.
 XX
 PF 29-OCT-2001; 2001GB-0025934.
 XX
 PR 23-SEP-1999; 99US-155493P.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99NO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-169232P.
 PR 22-SEP-2000; 2000GB-0023315.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 WPI: 2002-396337/43.

Best Local Similarity 99.7%; Pred. No. 5.3e-256;		Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	1	MLPGLALLLAATWATARALEVPTDGNAGLLAEQIAFMFCGRLNHMHNVQNGKWDSPSGTK	60
DB	1	MLPGLALLLAATWATARALEVPTDGNAGLLAEQIAFMFCGRLNHMHNVQNGKWDSPSGTK	60
QY	61	TCIDTKEGILQYCOEYVPEQITNVVEANOPTVIONMCKRGKCKTHPHFVPIRCLVG	120
DB	61	TCIDTKEGILQYCOEYVPELOITNVVEANOPTVIONMCKRGKCKTHPHFVPIRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR	180
DB	121	EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR	180
QY	181	GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE	240
DB	181	GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE	240
QY	241	EADDEDEDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDV	300
DB	241	EADDEDEDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDV	300
QY	301	DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEAKNLPKADKKAVIOHF	360
DB	301	DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEAKNLPKADKKAVIOHF	360
QY	361	QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK	420
DB	361	QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK	420
QY	421	KYVRAEQKORHTLKHFRHVRMVDPKKAQIRSOVNIHLRVIYERANOSLSLLYPAVA	480
DB	421	KYVRAEQKORHTLKHFRHVRMVDPKKAQIRSOVNIHLRVIYERANOSLSLLYPAVA	480
QY	481	EETODEVELLOKEQNSDDVLNMISEPRISYGNDAIMPSLTETKTVELLPVNGEFSJ	540
DB	481	EETODEVELLOKEQNSDDVLNMISEPRISYGNDAIMPSLTETKTVELLPVNGEFSJ	540
QY	541	DLOLPHSFGADSVANTENEVPDPAADRGLTIRPGSLTNIKTEIESEVNIADAF	600
DB	541	DLOLPHSFGADSVANTENEVPDPAADRGLTIRPGSLTNIKTEIESEVNIADAF	600
QY	601	RHDSGYEVHHQKLVFAEDVGNKGAIGLMVGGVVIATVITLVMKKKYTSIHHGV	660
DB	601	RHDSGYEVHHQKLVFAEDVGNKGAIGLMVGGVVIATVITLVMKKKYTSIHHGV	660
QY	661	VEYDAAVPEERHLSKMOQNGYENPTYKFEQONKK	697
DB	661	VEYDAAVPEERHLSKMOQNGYENPTYKFEQONKK	697
RESULT 9			
AAE10635			
ID	AAE10635 standard; Protein; 697 AA.		
XX			
AC	AAE10635;		
XX			
DT	10-DEC-2001 (first entry)		
XX			
DE	Human amyloid protein precursor 695-KK (APP695-KK) isoform.		
XX			
KW	Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;		
KW	Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;		
KW	amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective.		
XX			
OS	Home sapiens.		
OS	Synthetic.		
XX			
PN	GB237767-A.		
XX			
PD	04-JUL-2001.		
XX			
PF	22-SEP-2000;	2000GB-0023315.	
XX	23-SEP-1999;	99US-0155493.	
PR	23-SEP-1999;	99US-0404133.	
PR	23-SEP-1999;	99WC-US20881.	
PR	23-OCT-1999;	99US-0416901.	
PR	06-DEC-1999;	99US-0169232.	
XX	(P8AA)	PHARMACIA & UPJOHN CO.	
PI	Bienkowski MJ,	Guiney M;	
PI	WPI:	2501-444208/48.	
DR	N-PSDB;	AAD17871.	
XX	Polypeptide comprising fragments of human aspartyl protease with		
PI	amyloid precursor protein processing activity and alpha-secretase		
PI	activity, for identifying modulators useful in treating Alzheimer's		
PI	disease.		
XX	Example 6; Page 114-116; -87pp; English.		
PS	The patent discloses human aspartyl protease 1 (hu-Aspl) or modified		
CC	Aspl proteins which lack transmembrane domain or amino terminal		
CC	domain or cytoplasmic domain and retains alpha-secretase activity		
CC	and amyloid protein precursor (APP) processing activity. The proteins		
CC	of the invention are useful for assaying hu-Aspl alpha-secretase		
CC	activity, which in turn is useful for identifying modulators of		
CC	hu-Aspl alpha-secretase activity, where modulators that increase		
CC	hu-Aspl alpha-secretase activity are useful for treating Alzheimer's		
CC	disease (AD) which causes progressive dementia with consequent		
CC	neuronal loss. Hu-Aspl protease substrate is useful for assaying		
CC	hu-Aspl proteolytic activity, by contacting hu-Aspl protein with		
CC	the substrate under acidic conditions and determining the level of		
CC	hu-Aspl proteolytic activity. The present sequence is human amyloid		
CC	protein precursor 695-KK (APP695-KK) isoform which is obtained by		
CC	the addition of two Lys residues (KK motif) at the C-terminus of		
CC	APP695 protein.		
XX	Sequence 697 AA;		
SQ			
Query Match		99.8%; Score 3643; DB 22; Length 697;	
Best Local Similarity		99.7%; Pred. No. 5.3e-256;	
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MLPGLALLLAATWATARALEVPTDGNAGLLAEQIAFMFCGRLNHMHNVQNGKWDSPSGTK	60
DB	1	MLPGLALLLAATWATARALEVPTDGNAGLLAEQIAFMFCGRLNHMHNVQNGKWDSPSGTK	60
QY	61	TCIDTKEGILQYCOEYVPELOITNVVEANOPTVIONMCKRGKCKTHPHFVPIRCLVG	120
DB	61	TCIDTKEGILQYCOEYVPELOITNVVEANOPTVIONMCKRGKCKTHPHFVPIRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR	180
DB	121	EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR	180
QY	181	GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE	240
DB	181	GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE	240
QY	241	EADDEDEDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDV	300
DB	241	EADDEDEDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVRVPTTAASTPDV	300
QY	301	DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEAKNLPKADKKAVIOHF	360
DB	301	DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEAKNLPKADKKAVIOHF	360
QY	361	QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK	420
DB	361	QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK	420

QY 421 KYVRAEQKDRQHTLKHFHVMVDPKKAQAQIRSOVMTHLRVYVYERKNQOSLSLYNNPVA 480
 DB //
 QY 421 KYVRAEQKDRQHTLKHFHVMVDPKKAQAQIRSOVMTHLRVYVYERKNQOSLSLYNNPVA 480
 DB //
 QY 481 ERIQDEVDLLOKQNYSDOVLAKMISEPRISYNDALMPSLTETKTTVELLPVNGEESL 540
 DB //
 QY 481 ERIQDEVDLLOKQNYSDOVLAKMISEPRISYNDALMPSLTETKTTVELLPVNGEESL 540
 DB //
 QY 541 DDLQPHWSFGADSVPAANTENEVEVDPAADRLITRPGSGLNINTEISEVKNLDAEP 600
 DB //
 QY 541 DDLQPHWSFGADSVPAANTENEVEVDPAADRLITRPGSGLNINTEISEVKNLDAEP 600
 DB //
 QY 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLWGVVIAIVITLVMLKKQYTSIHGV 660
 DB //
 QY 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLWGVVIAIVITLVMLKKQYTSIHGV 660
 DB //
 QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
 DB //
 QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
 DB //

RESULT 10
 AA06865
 ID AA06865 standard; Protein: 697 AA.
 XX AA06865;
 AC AA06865;
 XX 23-OCT-2001 (first entry)
 XX Human amyloid precursor protein 695-KK (AP695-KK) isoform.
 DE
 XX Human: aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; glycosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neuroprotection;
 KW neuroprotective; antisense therapy; gene therapy; AP695-KK; mutant;
 KW mutain.
 XX
 OS Homo sapiens.
 XX
 XX WO200150829-A2.
 PN
 XX
 XX 19-JUL-2001.
 PD
 XX
 XX 09-MAY-2001; 2001WO-IB00799.
 PF
 XX
 XX 09-MAY-2001; 2001WO-IB00799.
 PK
 XX
 XX (BIEN//) BIENKOWSKI M J.
 PA (GURN//) GURNEY M E.
 PA (HEIN//) HEINIKSON R L.
 PA (PARO//) PARODI L A.
 PA (YANR//) YAN R.
 XX
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 PI
 XX WPI: 2001-483072/52.
 DR
 XX N-PSDB: AAD13027.
 DR
 XX
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX
 XX Example 6; Page 144-146; 195pp; English.
 PS
 XX
 XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.
 CC Human aspartyl proteases can act as beta-secretase proteases useful for
 CC treating Alzheimer's disease. APP isoforms are useful for identifying
 CC modulators of amyloid-beta peptide production, for use in designing
 CC therapeutics for the treatment and prevention of Alzheimer's disease.
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis

CC and neuronal loss. APP isoforms are also used in methods for identifying
 CC inhibitors and modulators of human Asp2 activity. The invention relates
 CC to a method for identifying agents that modulate the activity of human
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
 CC as a means to screen in cellular assays for the inhibitors of beta- and
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
 CC polymerase chain reactions (PCR). The probes are useful for detecting
 CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
 CC blots. The present sequence is modified human amyloid precursor
 CC protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
 CC addition of two Lys residues (KK motif) at the C-terminal end of APP695
 CC isoform.
 XX

QY Sequence 697 AA;

Query Match 99.8%; Score 3643; DB 22; Length 697;
 Best Local Similarity 99.7%; Pred. No. 53e-256;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPLGLALLLAANTARALEVPTDGNAGLLAEPOIAFMCGRLNMHNMVQNGKWDSPSGTK 60
 DB 1 MLPLGLALLLAANTARALEVPTDGNAGLLAEPOIAFMCGRLNMHNMVQNGKWDSPSGTK 60
 QY 61 TC:DTWKEGILQYCOEYVPELQITNVVEANQPTVIONWCKRGKCKOCTHPHFVPIRYCTVG 120
 DB 61 TCIDTWKEGILQYCOEYVPELQITNVVEANQPTVIONWCKRGKCKOCTHPHFVPIRYCTVG 120
 QY 121 EFVSDALLVPDKCKFLHOERMDVCEETHLHWHTVAKETCEKSTINLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHOERMDVCEETHLHWHTVAKETCEKSTINLHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWGGADTDYAGSDEKVVVEAEVEAEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWGGADTDYAGSDEKVVVEAEVEAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEYEAETERTTSIATTTTTSVSEVVEVRYPTTAASPTDAV 300
 DB 241 EADDDDEDDGDEVEEAEPEYEAETERTTSIATTTTTSVSEVVEVRYPTTAASPTDAV 300
 QY 301 DKYLETPGDNENHAFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 DB 301 DKYLETPGDNENHAFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 QY 361 QEKVESLEGEANERQOLVETIHARVEAMLDNRRLALENYITALQAVPPRRHVFENMLK 420
 DB 361 QEKVESLEGEANERQOLVETIHARVEAMLDNRRLALENYITALQAVPPRRHVFENMLK 420
 QY 421 KYVRAEQKDRQHTLKHFHVMVDPKKAQAQIRSOVMTHLRVYVYERKNQOSLSLYNNPVA 480
 DB 421 KYVRAEQKDRQHTLKHFHVMVDPKKAQAQIRSOVMTHLRVYVYERKNQOSLSLYNNPVA 480
 QY 481 ERIQDEVDLLOKQNYSDOVLAKMISEPRISYNDALMPSLTETKTTVELLPVNGEESL 540
 DB 481 ERIQDEVDLLOKQNYSDOVLAKMISEPRISYNDALMPSLTETKTTVELLPVNGEESL 540
 QY 541 DDLQPHWSFGADSVPAANTENEVEVDPAADRLITRPGSGLNINTEISEVKNLDAEP 600
 DB 541 DDLQPHWSFGADSVPAANTENEVEVDPAADRLITRPGSGLNINTEISEVKNLDAEP 600
 QY 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLWGVVIAIVITLVMLKKQYTSIHGV 660
 DB 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLWGVVIAIVITLVMLKKQYTSIHGV 660
 QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 1:
 AA06609
 ID AA06609 standard; Protein: 697 AA.
 XX AA06609;
 AC AA06609;

XX DT 24-OCT-2001 (first entry)
 XX DE Human Amyloid precursor protein mutant, APP695-KK.
 XX KW Human; Aspartyl protease; Asp2b; beta-secretase; neurotropic;
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
 KW amyloid-beta; Abeta; APP695-KK; mutant; mature.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FH Misc-difference 696, 697
 FT /note="2 Extra Lys residues added compared to
 FT wild-type APP695"
 XX WO200145098-A2.
 XX 12-JUL-2001.
 XX 09-MAY-2001; 2001WO-IB00798.
 XX 09-MAY-2001; 2001WO-IB00798.
 XX (BIEN/) BIENKOWSKI M J.
 XX (GJRN/) GURNEY M E.
 XX (HEIN/) HEINRIKSSON R L.
 XX (PARC/) PARODI L A.
 XX (YANK/) YAN R.
 XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
 XX WPI: 2001-502549/55.
 XX N-PSDB: AAS1523.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl-
 XX protease 2, lacking Asp2 transmembrane domain and retaining beta
 XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
 XX activity -
 XX Example 6; Page 144-146; 185pp; English.
 XX The invention relates to a purified polypeptide comprising a fragment of
 XX mammalian aspartyl protease (Asp2) protein which lacks the Asp2
 XX transmembrane domain and the Asp2 protein, and where the polypeptide and
 XX the fragment retain the beta-secretase activity of the mammalian Asp2
 XX protein. The invention also details polynucleotides for the Asp
 XX proteins and vectors expressing them, and a polypeptide (isoform of
 XX amyloid protein precursor (APP)) comprising the amino acid sequence of an
 XX APP or its fragment containing an APP cleavage site recognizable by a
 XX mammalian beta-secretase, and further comprising two lysine residues at
 XX the carboxyl terminus of the amino acid sequence of the mammalian APP or
 XX APP fragment. Also included in the invention are methods of identifying
 XX modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 XX useful for treating Alzheimer's disease. APP is useful in methods for
 XX identifying inhibitors or modulators of human Asp2 activity and
 XX amyloid-beta (beta) peptide production. APP is also useful in designing
 XX therapeutics for the treatment or prevention of Alzheimer's disease.
 XX APP comprising the APP-Sw-beta-secretase peptide sequence (NDA), which
 XX is associated with increased levels of Abeta processing is useful in
 XX assays relating to the Alzheimer's research. The expression vector is useful
 XX for recombinantly expressing APP. Nucleic acids that hybridize to
 XX Asp oligonucleotides are useful as probes or primers. The probes are
 XX useful for detecting Hu-Asp nucleic acids in *in vitro* assays and in
 XX Northern and Southern blots. The present sequence is the human
 XX APP695 mutant. APP695-KK which has 2 extra Lys residues added at
 XX the C-terminus compared to the wild-type APP695. The mutation alters the
 XX specificity of the APP gamma-secretase activity and increases the rate
 XX of processing of the amyloid Abeta peptide.

Query Match 99.8%; Score 3643; DB 22; Length 697;

Best Local Similarity 99.7%; Pred. No. 5.3e-256;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLAALLLAAMTARALEVPTDGNAGLLAEPDIAAMFCGRLNMHMVQNGKWDSDSGTK 60
 DB 1 MLPGLAALLLAAMTARALEVPTDGNAGLLAEPDIAAMFCGRLNMHMVQNGKWDSDSGTK 60
 QY 61 TCIDTKHGIILOYCOEYVPELQITNNVEANQPV71ONMCKKGRKCKOCTHPIHVPYHCLWG 120
 DB 61 TCIDTKHGIILOYCOEYVPELQITNNVEANQPV71ONMCKKGRKCKOCTHPIHVPYHCLWG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVYVEAEVEEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVYVEAEVEEVEE 240
 QY 241 EAUDDEDDGDEVEHEAEPEEYEAETRTISIAITTTITTESVEEVVVP7TAASPTDAY 300
 DB 241 EAUDDEDDGDEVEHEAEPEEYEAETRTISIAITTTITTESVEEVVVP7TAASPTDAY 300
 QY 301 DKYLETPGDNEHAHFQKAKERLEAKHRRSMQVMEWEAEAEQAKNLPKADKKAVIQHF 360
 DB 301 DKYLETPGDNEHAHFQKAKERLEAKHRRSMQVMEWEAEAEQAKNLPKADKKAVIQHF 360
 QY 361 QEKVESLEQEAANERQQLVETHKARVAMLNDRRRLALENYITALQAVPPRPHVNMUK 420
 DB 361 QEKVESLEQEAANERQQLVETHKARVAMLNDRRRLALENYITALQAVPPRPHVNMUK 420
 QY 421 KYVRAEQKDRQHTLKHFHVRMYDPKKAQIRSOVMTLRVLYERNQSLSLLYNPVAVA 480
 DB 421 KYVRAEQKDRQHTLKHFHVRMYDPKKAQIRSOVMTLRVLYERNQSLSLLYNPVAVA 480
 QY 481 EE-ODEYDELLQKPNYSDDVLANMISEPRISYGNDAIMP5LTFETKTVELLVPNGEFS 540
 DB 481 EEIQDEYDELLQKPNYSDDVLANMISEPRISYGNDAIMP5LTFETKTVELLVPNGEFS 540
 QY 541 DDLOPHSFSGADSVPAANTENEVEPVDARPAADRLTTRPGSLTNIKTEISEVNLD 600
 DB 541 DDLOPHSFSGADSVPAANTENEVEPVDARPAADRLTTRPGSLTNIKTEISEVNLD 600
 QY 561 RHDSGYEVHVKQLVFAEDYGSNKGALIGLVGSGVVIATVIVILYMKKKOYTSIHGV 660
 DB 561 RHDSGYEVHVKQLVFAEDYGSNKGALIGLVGSGVVIATVIVILYMKKKOYTSIHGV 660
 QY 661 VEVDAAVTPBERHLSKMQQNGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPBERHLSKMQQNGYENPTYKFFEQMONKK 697
 RESULT 12
 AAU07208
 ID AAU07208 standard; Protein; 697 AA.
 XX AAU07208;
 XX 24-OCT-2001 (first entry)
 XX Human beta-amyloid protein precursor, APP695-KK.
 XX Human; aspartyl protease 1; Asp-1; neurotropic; neuroprotective;
 XX aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 XX beta-secretase; Alzheimer's disease; APP695-KK.
 XX Homo sapiens.
 XX WO200145097-A2.
 XX 12-JUL-2001.
 XX 09-MAY-2001; 2001WO-IB00797.

XX 09-MAY-2001: 2001WO-IB00797.
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURNEY/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX WPI: 2001-502548/55.
 DR N-PSDB: AAS11708.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX Example 6: Page 144-146; 185pp; English.
 XX The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP),
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognizable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP695-KK,
 CC used in the method of the invention.
 XX Sequence 597 AA;
 SQ
 Query Match: 99.8%; Score 3643; LB 22; Length 697;
 Best Local Similarity 99.7%; Pred. No. 5.3e-256;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAATAARAEVPTDGNAGLLAEPOIAMFCGRLENNHNVGNCKWDSPPSGTK 60
 DB 1 MLPGLALLLAATAARAEVPTDGNAGLLAEPOIAMFCGRLENNHNVGNCKWDSPPSGTK 60
 QY 61 TCIDTREGILQYQEVYFELQIINVEANQPTVIONKCKRGRKQCKTHPHFVYPCVLG 120
 DB 61 TCIDTREGILQYQEVYFELQIINVEANQPTVIONKCKRGRKQCKTHPHFVYPCVLG 120
 QY 121 EFVSDALLVPDKCKFLHCHQRMVDCVTHLHHVYAKETCSKSTNLHDYGNLLPCGIDKPR 180
 DB 121 EFVSDALLVPDKCKFLHCHQRMVDCVTHLHHVYAKETCSKSTNLHDYGNLLPCGIDKPR 180
 QY 181 GVEFVCCPLAEESDNDVSDADEDDSDVWGGADTDYADGSEKVVVEAESEVALEVEE 240
 DB 181 GVEFVCCPLAEESDNDVSDADEDDSDVWGGADTDYADGSEKVVVEAESEVALEVEE 240
 QY 241 EADDDEDDGDEVEEAEPEEATERTISTATITTTTIESVEEVVPTTAASTPDVAV 300
 DB 241 EADDDEDDGDEVEEAEPEEATERTISTATITTTTIESVEEVVPTTAASTPDVAV 300
 QY 301 DKYLETPGDENAHAFKAKERLEAKHRMRMSQVMREWEAEAEQAKNLFKADKAVIQHF 360
 DB 301 DKYLETPGDENAHAFKAKERLEAKHRMRMSQVMREWEAEAEQAKNLFKADKAVIQHF 360

CY 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHHVFNMLK 420
 DB 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHHVFNMLK 420
 QY 421 KYVRAEKDRQHTLKHFEHVRMVDPKKAAQIISQVMTHLRVIVYERMNQSLSLLYNPFAVA 480
 DB 421 KYVRAEKDRQHTLKHFEHVRMVDPKKAAQIIRSOVMTHLRVIVYERMNQSLSLLYNPFAVA 480
 QY 481 FELODEYDELIQKQDNYSDDVLANMISEPRISYGNDAIMPSSL:ETKTTIVEILLPNGEFSL 540
 DB 481 ESIQDEYDELIQKQDNYSDDVLANMISEPRISYGNDAIMPSSL:ETKTTIVEILLPNGEFSL 540
 QY 541 DDLQPHWISFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNINIKETISEVNLDAEF 600
 DB 541 DDLQPHWISFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNINIKETISEVNLDAEF 600
 QY 601 RHDGSEYVHHOKLVFFAEDVGSNGKGAIGLMVGWGVIAIVITVLMKKQYTSIHGV 660
 DB 601 RHDGSEYVHHOKLVFFAEDVGSNGKGAIGLMVGWGVIAIVITVLMKKQYTSIHGV 660
 QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMONKK 697
 RESULT 13
 AAEE02587
 ID AAE02587 standard; Protein: 697 AA.
 XX AAE02587;
 XX 10-AUG-2001 (first entry)
 DE Human amyloid precursor protein 695-KK (APP695-KK).
 KW Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
 therapy; Alzheimer's disease; antialzheimer's.
 OS Homo sapiens.
 CS Synthetic.
 XX WO200123533-A2.
 XX 05-APR-2001.
 XX 22-SEP-2000; 2000WO-US26080.
 XX 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX (PIAA) PHARMACIA & UPJOHN CO.
 XX Gurney M, Bienkowski MJ;
 WPI: 2001-290516/30.
 DR N-PSDB: AAD06745.
 XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease -
 XX Example 6: Page 143-145; 189pp; English.
 XX The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human APP695-KK. This
 CC sequence contains two carboxy-terminal lysine residues.

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SQ      Sequence      697 AA;
Query Match      99.8%; Score 3643; DB 23; Length 697;
Best Local Similarity 99.7%; Pred. No. 5.3e-256;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLNHNMVQNGKWDSPSGTK 60
Db      1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLNHNMVQNGKWDSPSGTK 60

Qy      61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120
Db      61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120

Qy      121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCCGIDKFR 180
Db      121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCCGIDKFR 180

Qy      181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSECKVVEVAEEVEAEVEE 240
Db      181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSECKVVEVAEEVEAEVEE 240

Qy      241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTITTESVEEVVRVPTTAASPDAY 300
Db      241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTITTESVEEVVRVPTTAASPDAY 300

Qy      301 DKYLETGPDENEHAFKAKERLEAKHREMSOVMEWEAEACAKNLPKAKKAVIQHF 360
Db      301 DKYLETGPDENEHAFKAKERLEAKHREMSOVMEWEAEACAKNLPKAKKAVIQHF 360

Qy      361 QEKVESLEQEAANEKQOLVETHMARVEAMLNDRRRLALENYITALQAVPRPRHVFNMCK 420
Db      361 QEKVESLEQEAANEKQOLVETHMARVEAMLNDRRRLALENYITALQAVPRPRHVFNMCK 420

Qy      421 KYRAEOKDQKHLKHFHYRMVDPKAAQIRSQVMTHLPIVIERMNSLSLLYNPAVA 480
Db      421 KYRAEOKDQKHLKHFHYRMVDPKAAQIRSQVMTHLPIVIERMNSLSLLYNPAVA 480

Qy      481 EETQDEVDLQKSONYSDCVLANMISEPRIYSGNDALMPSLTETKTIVELLVNGEFSL 540
Db      481 EETQDEVDLQKSONYSDCVLANMISEPRIYSGNDALMPSLTETKTIVELLVNGEFSL 540

Qy      541 DDQPHSFSGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKIEISVNLDAEF 600
Db      541 DDQPHSFSGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKIEISVNLDAEF 600

Qy      601 RHDGSEVHHQKLVFAEDVCSNKGAIGLWGGVVIATVITLWMLKKQYTSIHGV 660
Db      601 RHDGSEVHHQKLVFAEDVCSNKGAIGLWGGVVIATVITLWMLKKQYTSIHGV 660

Qy      661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
Db      661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 14
ID      ABB78596
XX      ABB78596 standard; Protein: 697 AA.
AC      ABB78596;
XX      16-JUL-2002 (first entry)
XX      Human APP695-KK protein sequence SEQ ID NO:16.
XX      Human: Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW      proteolytic; amyloid precursor protein; APP.
XX      Homo sapiens.
CS      G82367060-A.
PN      27-MAR-2002.
XX      27-MAR-2002.

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XX      29-OCT-2001; 2001GB-0025934.
PF      23-SEP-1999; 59US-155493P.
XX      23-SEP-1999; 59US-0404133.
PR      23-SEP-1999; 59WO-US20881.
PR      13-OCT-1999; 99US-0416901.
PR      06-DEC-1999; 99US-169232P.
PR      22-SEP-2000; 2000GB-0023315.
XX      (PHAA ) PHARMACIA & UPJOHN CO.
PA      Blenkowski MJ, Gurney M;
XX      WPI: 2002-396337/43.
PI      N-PSDB: AB152463.
XX      Human aspartyl protease 1 substrates useful in assays to detect
PT      aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
XX      disease.
XX      Example 6: Page 114-116; 182pp; English.
XX      The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC      substrate (I) which comprises a peptide of no more than 50 amino acids,
CC      and which comprises the 6 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC      Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC      proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC      (1) under acidic conditions; and (b) determining the level of hu-Asp1
CC      proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC      nucleotide sequence that hybridises under stringent conditions to the
CC      non-coding strand complementary to a defined 1804 nucleotide sequence
CC      (see AB152456) where the nucleotide sequence encodes a polypeptide having
CC      Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC      domain; (3) a purified polynucleotide (III') comprising a sequence that
CC      hybridises under stringent conditions to (III) (the nucleotide sequence
CC      encodes a polypeptide further lacking a pro-peptide domain corresponding
CC      to amino acids 23-62 of hu-Asp1 (see AB878589)); (4) a vector (IV)
CC      comprising (III) or (III'); and (5) a host cell (V) transformed or
CC      transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC      aspartyl protease activity, (II) and therefore diagnose diseases
CC      associated with aberrant hu-Asp1 expression and activity such as
CC      Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC      hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC      sequence represents human amyloid precursor protein APP695-KK, which is
CC      given in an example from the present invention.
XX      Sequence 697 AA;
Query Match      99.8%; Score 3643; DB 23; Length 697;
Best Local Similarity 99.7%; Pred. No. 5.3e-256;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLNHNMVQNGKWDSPSGTK 60
Db      1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLNHNMVQNGKWDSPSGTK 60

Qy      61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120
Db      61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120

Qy      121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCCGIDKFR 180
Db      121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCCGIDKFR 180

Qy      181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSECKVVEVAEEVEAEVEE 240
Db      181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSECKVVEVAEEVEAEVEE 240

Qy      241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTITTESVEEVVRVPTTAASPDAY 300
Db      241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTITTESVEEVVRVPTTAASPDAY 300

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QY 301 DKYLETGCDENEHAHFQKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETGCDENEHAHFQKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVDPKKAQAQIRSQVMTLRLVIYERMNQSLLLYNPVAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRVDPKKAQAQIRSQVMTLRLVIYERMNQSLLLYNPVAVA 480
QY 481 BEIQDEVEDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSEVNLDAEF 540
DB 481 BEIQDEVEDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSEVNLDAEF 540
QY 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTPGSGSLTNIKTEEISEVNLDAEF 600
DB 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTPGSGSLTNIKTEEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 15
RAY88435
ID AAY88435 standard; Protein: 695 AA.
XX
AC AAY88435;
XX
DI 03-AUG-2000 (first entry)
XX
DE Human APP695-sw variant amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site.
XX
OS Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 59WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;
XX
DR WPI: 2000-303209/26.
DR N-PSDB; AAA15672.
XX
XX
PT New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at:
PT the beta secretase site to produce amyloid beta peptide -
XX
PS Example 6; Page 125-129; 183pp; English.
XX
XX
CC This sequence represents a human amyloid precursor protein 695 (APP695)
CC variant amino acid sequence. The sequence is used in an example of the
CC invention, showing that modification of APP can increase beta amyloid
CC peptide processing. The invention relates to a protease (e.g. Asp2)
CC capable of cleaving the beta secretase site of amyloid precursor protein
CC (APP). The protease contains a sequence encoding the amino acid sequence
CC DTG and a sequence encoding DSG or DIG separated by 100-300 amino acids.
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CC When mutated the APP gene causes an autosomal dominant form of
CC Alzheimer's disease. APP localises to the cell surface membrane and have
CC a single C-terminal transmembrane domain. Proteolytic processing of APP
CC produces the amyloid beta protein, which is possibly very important in
CC Alzheimer's disease. The invention includes a nucleotide sequence
CC encoding the protease, a vector containing the nucleotide sequence, and a
CC cell line comprising the vector. Methods for screening for inhibitors of
CC beta secretase activity are also given in the invention. The human
CC aspartase protein and nucleotide sequences and the methods for
CC identifying inhibitors of the protease, are useful in the treatment of
CC and research in to Alzheimer's disease.
```

XX Sequence 695 AA;

Query Match: 99.7%; Score 3641; DB 21; Length 695;
Best local Similarity 100.0%; Pred. No. 7.4e-256;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MLPGCLALLLLAANTARALEVPTDGNAGLLAEPOIAMEFCGRLNHMHVYQNGKWDSPSGTK 60
DB 1 MLPGCLALLLLAANTARALEVPTDGNAGLLAEPOIAMEFCGRLNHMHVYQNGKWDSPSGTK 60
QY 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIQNMCKRGRKOCKTHPHFVPRCLVG 120
DB 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIQNMCKRGRKOCKTHPHFVPRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTYAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTYAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEEVEE 240
QY 241 EAUDDEDDEGDEVEEAEPEYEATEKITTSIATTTTTTTSVESVEVVRVPTAASTPDV 300
DB 241 EAUDDEDDEGDEVEEAEPEYEATEKITTSIATTTTTTTSVESVEVVRVPTAASTPDV 300
QY 301 DKYLETGCDENEHAHFQKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETGCDENEHAHFQKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVDPKKAQAQIRSQVMTLRLVIYERMNQSLLLYNPVAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRVDPKKAQAQIRSQVMTLRLVIYERMNQSLLLYNPVAVA 480
QY 481 BEIQDEVEDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSEVNLDAEF 540
DB 481 BEIQDEVEDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSEVNLDAEF 540
QY 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTPGSGSLTNIKTEEISEVNLDAEF 600
DB 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTPGSGSLTNIKTEEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695
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Job time : 40.3333 secs

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OM protein - protein search, using sw model

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(without alignments)
1638.370 Million cell updates/sec

Title: US-09-806-194-18
Perfect score: 3651
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Scoring table: BLOSUM62
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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep: *
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6: /cgn2.6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3651	100.0	697	4	US-09-548-372D-18
2	3651	100.0	697	4	US-09-548-367D-18
3	3651	100.0	697	4	US-09-551-853D-18
4	3643	99.8	697	4	US-09-548-372D-16
5	3643	99.8	697	4	US-09-548-367D-16
6	3643	99.8	697	4	US-09-551-853D-16
7	3641	99.7	595	4	US-09-548-372D-12
8	3641	99.7	595	4	US-09-548-367D-12
9	3641	99.7	595	4	US-09-551-853D-12
10	3638	99.6	597	4	US-09-548-372D-20
11	3638	99.6	597	4	US-09-548-367D-20
12	3638	99.6	597	4	US-09-551-853D-20
13	3633	99.5	695	1	US-09-123-702-2
14	3633	99.5	695	2	US-08-104-165-1
15	3633	99.5	695	3	US-08-464-250-1
16	3633	99.5	695	4	US-08-464-250-1
17	3633	99.5	695	4	US-09-458-481A-7
18	3633	99.5	695	4	US-09-458-481B-8
19	3633	99.5	695	4	US-09-548-372D-10
20	3633	99.5	695	4	US-09-548-367D-10
21	3633	99.5	695	4	US-09-551-853D-10
22	3633	99.5	695	6	5218100-2
23	3628	99.4	695	4	US-09-548-372D-14
24	3628	99.4	695	4	US-09-548-367D-14
25	3628	99.4	695	4	US-09-551-853D-14
26	3627	99.3	694	1	US-08-339-152A-18
27	3627	99.3	694	2	US-08-007-999B-5

29	3627	99.3	694	2	US-08-689-276A-5	Sequence 5, Appl
29	3621	99.2	695	1	US-08-371-830-27	Sequence 27, Appl
30	3621	99.2	695	5	PCT-US94-01712-27	Sequence 27, Appl
31	3609	98.8	695	1	US-08-339-152A-30	Sequence 30, Appl
32	3604	98.7	753	4	US-09-548-372D-61	Sequence 61, Appl
33	3604	98.7	753	4	US-09-548-367D-61	Sequence 61, Appl
34	3604	98.7	753	4	US-09-551-853D-61	Sequence 61, Appl
35	3594	98.4	751	1	US-08-123-702-4	Sequence 4, Appl
36	3594	98.4	751	2	US-08-104-165-2	Sequence 2, Appl
37	3594	98.4	751	2	US-08-422-333-2	Sequence 2, Appl
38	3594	98.4	751	2	US-08-422-333-21	Sequence 21, Appl
39	3594	98.4	751	3	US-08-464-250-2	Sequence 2, Appl
40	3594	98.4	751	4	US-08-464-250-2	Sequence 5, Appl
41	3594	98.4	751	4	US-08-832-867-5	Sequence 57, Appl
42	3594	98.4	751	4	US-09-548-372D-57	Sequence 57, Appl
43	3594	98.4	751	4	US-09-548-367D-57	Sequence 57, Appl
44	3594	98.4	751	4	US-09-551-853D-57	Sequence 57, Appl
45	3594	98.4	751	6	5187153-2	Patent No. 5187153

ALIGNMENTS

RESULT 1
US-09-548-372D-18
: Sequence 18, Application US/09548372D
: Patent No. 6420334
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
: FILE REFERENCE: 29915/62801
: CURRENT APPLICATION NUMBER: US/09/548.372D
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patent In version 3.1
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRI
: ORGANISM: Homo sapiens
US-09-548-372D-18

Query Match	100.0%	Score	3651	DB 4	Length	697	
Best Local Similarity	100.0%	Pred. No.	3.1e+265	Indels	0	Gaps	0
Matches	697	Conservative	0	Mismatches	0		

QY	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAFMCGRLNMHMNVQNGKWDSPGSK	60
DB	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAFMCGRLNMHMNVQNGKWDSPGSK	60
QY	61	TCIDTKGGLQYCGEVVPELOITNNVEANQPVITONMCKRGKCKKTHPHVPIYRCLVG	120
DB	61	TCIDTKGGLQYCGEVVPELOITNNVEANQPVITONMCKRGKCKKTHPHVPIYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHOERMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPGIDKFR	180
DB	121	EFVSDALLVPDKCKFLHOERMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPGIDKFR	180
QY	181	GVFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE	240
DB	181	GVFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE	240
QY	241	EADDEDDEGDEVEEAEPEEATERTTSTIATTTTTTSTESVEEVVPTTAASTPDV	300
DB	241	EADDEDDEGDEVEEAEPEEATERTTSTIATTTTTTSTESVEEVVPTTAASTPDV	300

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QY 301 DKYLETPGDNENAHFQKAKERLEAKHRRMSQVREWEAEARQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDNENAHFQKAKERLEAKHRRMSQVREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
Db 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFHVRVMDPKAAQIRSQVMTHLRVYIERMNSQSLSLYNNPVA 480
Db 421 KYVRAEQKDRQHTLKHFHVRVMDPKAAQIRSQVMTHLRVYIERMNSQSLSLYNNPVA 480
QY 481 BEIQDEVDELLOKEQNYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Db 481 BEIQDEVDELLOKEQNYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDLOPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVNLDAEF 600
Db 541 DDLOPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697

RESULT 2
US-09-548-367D-18
; Sequence 18, Application US/09545367D
; Patent No. 6440598
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/628CH
; CURRENT APPLICATION NUMBER: US/09/548.367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 03/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-18

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 3,le-255;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVNEANOPVTIQNCKRGRKQCKTHPHFVPIRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELQITNVNEANOPVTIQNCKRGRKQCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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QY 181 GYFVCCPLAESDNDVSADAEUDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEER 240
Db 181 GYFVCCPLAESDNDVSADAEUDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEER 240
QY 241 EADDDDEDSDSDEVEEAEPEEYEEATERITTSIATTTTTSVEEVRVPTTAASTPDVAV 300
Db 241 EADDDDEDSDSDEVEEAEPEEYEEATERITTSIATTTTTSVEEVRVPTTAASTPDVAV 300
QY 301 DKYLETPGDNENAHFQKAKERLEAKHRRMSQVREWEAEARQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDNENAHFQKAKERLEAKHRRMSQVREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
Db 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFHVRVMDPKAAQIRSQVMTHLRVYIERMNSQSLSLYNNPVA 480
Db 421 KYVRAEQKDRQHTLKHFHVRVMDPKAAQIRSQVMTHLRVYIERMNSQSLSLYNNPVA 480
QY 481 BEIQDEVDELLOKEQNYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Db 481 BEIQDEVDELLOKEQNYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDLOPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVNLDAEF 600
Db 541 DDLOPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697

RESULT 3
US-09-551-853D-18
; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-18

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 3,le-265;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVNEANOPVTIQNCKRGRKQCKTHPHFVPIRCLVG 120
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; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-16

Query Match      99.8%: Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%: Pred. No. 1.2e-264;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAPQIAFPGHNMHNQVNGKWSDPGSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAPQIAFPGHNMHNQVNGKWSDPGSGTK 60
QY 61 TCIDTKEGILQCYQEVYPELOITNVVEANQPVTTQNMCKRGKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQCYQEVYPELOITNVVEANQPVTTQNMCKRGKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLQHERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLQHERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
DB 241 EADDEDEDDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMKEEAERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMKEEAERQAKNLPKADKAVIQHF 360
QY 361 QKVESLEQEAANERQOVLVETHMARVEAMNDRRRLALENYITALQAVPPRPRHVENMLK 420
DB 361 QKVESLEQEAANERQOVLVETHMARVEAMNDRRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFHEHVRMVDPKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFHEHVRMVDPKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
QY 481 EETQDEVDLQKEQNSYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
DB 481 EETQDEVDLQKEQNSYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
QY 541 DDLQPMHSEFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKNDAEF 600
DB 541 DDLQPMHSEFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKNDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVIAIVITLVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVIAIVITLVMLKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697

RESULT 6
US-09-551-853D-16
; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551.853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR FILING DATE: 2000-04-18
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
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; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101.594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-16

Query Match      99.8%: Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%: Pred. No. 1.2e-264;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAFPGRLNMHNQVNGKWDSPGSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAFPGRLNMHNQVNGKWDSPGSGTK 60
QY 61 TCIDTKEGILQCYQEVYPELOITNVVEANQPVTTQNMCKRGKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQCYQEVYPELOITNVVEANQPVTTQNMCKRGKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLQHERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLQHERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
DB 241 EADDEDEDDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMKEEAERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMKEEAERQAKNLPKADKAVIQHF 360
QY 361 QKVESLEQEAANERQOVLVETHMARVEAMNDRRRLALENYITALQAVPPRPRHVENMLK 420
DB 361 QKVESLEQEAANERQOVLVETHMARVEAMNDRRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFHEHVRMVDPKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFHEHVRMVDPKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
QY 481 EETQDEVDLQKEQNSYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
DB 481 EETQDEVDLQKEQNSYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
QY 541 DDLQPMHSEFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKNDAEF 600
DB 541 DDLQPMHSEFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKNDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVIAIVITLVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVIAIVITLVMLKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697

RESULT 7
US-09-548-372D-12
; Sequence 12, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
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FILE REFERENCE: 29915/52801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20681
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-12

Query Match
Best Local Similarity 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCVIG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCVIG 120
QY 121 EFVSALLVPDKCKFLHQRMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPGCIDKFR 180
DB 121 EFVSALLVPDKCKFLHQRMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDCKVVEVAEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDCKVVEVAEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTTTTSVEEVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTTTTSVEEVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRMSQVNRWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHRMSQVNRWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
QY 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLVNGEFSL 540
DB 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLVNGEFSL 540
QY 541 DDLQPHWSEFGADSVPAANTEVEPVDAARPAADRGLTTRPGSLTNKITEEISEVNLDAEF 600
DB 541 DDLQPHWSEFGADSVPAANTEVEPVDAARPAADRGLTTRPGSLTNKITEEISEVNLDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLVGGVVIATVITVLMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMN 695
DB 661 VEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMN 695

Query Match
Best Local Similarity 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCVIG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCVIG 120
QY 121 EFVSALLVPDKCKFLHQRMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPGCIDKFR 180
DB 121 EFVSALLVPDKCKFLHQRMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDCKVVEVAEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDCKVVEVAEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTTTTSVEEVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTTTTSVEEVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRMSQVNRWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHRMSQVNRWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
QY 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLVNGEFSL 540
DB 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLVNGEFSL 540
QY 541 DDLQPHWSEFGADSVPAANTEVEPVDAARPAADRGLTTRPGSLTNKITEEISEVNLDAEF 600
DB 541 DDLQPHWSEFGADSVPAANTEVEPVDAARPAADRGLTTRPGSLTNKITEEISEVNLDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLVGGVVIATVITVLMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMN 695
DB 661 VEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMN 695
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DB 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQINSQVYTHLHVYERKMOSLSLLYNVPAVA 480
QY 481 EBIQEVDELQKQYNSDDVLANNMISPRISYNDALMPSLTKTTESEVNLDAEF 540
DB 481 EBIQEVDELQKQYNSDDVLANNMISPRISYNDALMPSLTKTTESEVNLDAEF 540
QY 541 DDLQPHSFGADSVANTENEVEPVDPARPAADRGTLTPGSGGLINIKTEESEVNLDAEF 600
DB 541 DDLQPHSFGADSVANTENEVEPVDPARPAADRGTLTPGSGGLINIKTEESEVNLDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 11

US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-20

Query Match 99.6%; Score 3638; DB 4; Length 697;
Best Local Similarity 99.6%; Pred. No. 2.9e-264;
Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWSDPGSK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWSDPGSK 60
QY 61 TCIDTKEGILQCYQEVPELQITNVVEANQPTVTONWCKRGKCKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQCYQEVPELQITNVVEANQPTVTONWCKRGKCKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVVCETHLHWHTVAKETCSEKSTNLHDYGMILLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVVCETHLHWHTVAKETCSEKSTNLHDYGMILLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSDKVVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSDKVVVEAEVEAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEEAEIERTTSTATTTTTFESVEVVRVPIAATSTPDVAV 360
DB 241 EADDDEDDGDEVEEAEPEEAEIERTTSTATTTTTFESVEVVRVPIAATSTPDVAV 360
QY 301 DKYLETPGDENEHAFOKAKERLEAKHRMSQVNRWEBAERQAKNLPKADKKAVIGHF 360

DB 301 DKYLETPGDENEHAFOKAKERLEAKHRMSQVNRWEBAERQAKNLPKADKKAVIGHF 360
QY 361 QEKVESLEQEAANERQQLVETIMAKVEAMLNDRRLALENYIT:ALQAVPPRPRHVFNMKL 420
DB 361 QEKVESLEQEAANERQQLVETIMAKVEAMLNDRRLALENYIT:ALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRKSOVMTHLRVLYERKMOSLSLLYNVPAVA 480
DB 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRKSOVMTHLRVLYERKMOSLSLLYNVPAVA 480
QY 481 EBIQEVDELQKQYNSDDVLANNMISPRISYNDALMPSLTKTTESEVNLDAEF 540
DB 481 EBIQEVDELQKQYNSDDVLANNMISPRISYNDALMPSLTKTTESEVNLDAEF 540
QY 541 DDLQPHSFGADSVANTENEVEPVDPARPAADRGTLTPGSGGLINIKTEESEVNLDAEF 600
DB 541 DDLQPHSFGADSVANTENEVEPVDPARPAADRGTLTPGSGGLINIKTEESEVNLDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEDVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 12

US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20891
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-20

Query Match 99.6%; Score 3638; DB 4; Length 697;
Best Local Similarity 99.6%; Pred. No. 2.9e-264;
Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWSDPGSK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWSDPGSK 60
QY 61 TCIDTKEGILQCYQEVPELQITNVVEANQPTVTONWCKRGKCKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQCYQEVPELQITNVVEANQPTVTONWCKRGKCKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVVCETHLHWHTVAKETCSEKSTNLHDYGMILLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVVCETHLHWHTVAKETCSEKSTNLHDYGMILLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSDKVVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSDKVVVEAEVEAEVEE 240

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QY 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
DB 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENHAFHOKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVICHF 360
DB 301 DKYLETPGDENHAFHOKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVICHF 360
QY 361 QKVSLEQOEAERQOVLVTHMARVEAMLDNRRLALENYITAIQAVPPRPRHVFNMKL 420
DB 361 QKVSLEQOEAERQOVLVTHMARVEAMLDNRRLALENYITAIQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQKDROHTLKHFEIHRVMDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
DB 421 KYVRAEQKDROHTLKHFEIHRVMDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
QY 481 BEIQDEVELLOKEONYSDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
DB 481 BEIQDEVELLOKEONYSDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
QY 541 DOLQPHSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGITNKTESIYVNDJAEF 600
DB 541 DOLQPHSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGITNKTESIYVNDJAEF 600
QY 601 RHDSGYEVHHOKLVFFAEEDVGSNGKAIIGLMVGGVVIATVITLVMLKKQKTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEEDVGSNGKAIIGLMVGGVVIATVITLVMLKKQKTSIHGV 660
QY 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMKNK 695
DB 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMKNK 697
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RESULT 13
US-08-123-702-2
: Sequence 1. Application US/09123702
: Patent No. 5604131
: GENERAL INFORMATION:
: APPLICANT: Wadsworth, Samuel
: APPLICANT: Snyder, Benjamin
: APPLICANT: Reddy, Vermuri, B.
: APPLICANT: Wei, Chamer
: TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770
: Patent No. 5604131
: TITLE OF INVENTION: Containing a Genomic DNA Insert of the Kf and CX-2 Regions
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrea L. Pabst
: STREET: 2800 One Atlantic Center
: CITY: Atlanta
: STATE: GA
: COUNTRY: USA
: ZIP: 30309-3450
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/123,702
: FILING DATE: 17-SEPT-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: TS1121
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404)-873-8794
: TELEFAX: (404)-873-8795
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
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: LENGTH: 695 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-123-702-2
Query Match: 99.5%; Score 3633; DB 1; Length 695;
Rest Local Similarity 99.7%; Pred. No. 6.9e-264;
Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 MLPGALALLAAWTAARALEVPTDGNAGILAPPOIAMFCGRILNMHNVONGKWDSDPSGTK 60
DB 1 MLPGALALLAAWTAARALEVPTDGNAGILAPPOIAMFCGRILNMHNVONGKWDSDPSGTK 60
QY 61 TCIDTREGTIOYQCQVYPELQITNVVEANQVPTIQNMCKRGKCKOCTHPIHPIYRCLVG 120
DB 61 TCIDTREGTIOYQCQVYPELQITNVVEANQVPTIQNMCKRGKCKOCTHPIHPIYRCLVG 120
QY 121 EFVSALLVPDKCKFLHQRMDVCEHLHWHYAKETSEKSTNLHDYGMLLPGIDIKFR 180
DB 121 EFVSALLVPDKCKFLHQRMDVCEHLHWHYAKETSEKSTNLHDYGMLLPGIDIKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVYMGADTDYADGSEDKYVEVAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVYMGADTDYADGSEDKYVEVAEVEEVAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
DB 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENHAFHOKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVICHF 360
DB 301 DKYLETPGDENHAFHOKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVICHF 360
QY 361 QKVSLEQOEAERQOVLVTHMARVEAMLDNRRLALENYITAIQAVPPRPRHVFNMKL 420
DB 361 QKVSLEQOEAERQOVLVTHMARVEAMLDNRRLALENYITAIQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQKDROHTLKHFEIHRVMDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
DB 421 KYVRAEQKDROHTLKHFEIHRVMDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPVA 480
QY 481 BEIQDEVELLOKEONYSDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
DB 481 BEIQDEVELLOKEONYSDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
QY 541 DOLQPHSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGITNKTESIYVNDJAEF 600
DB 541 DOLQPHSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGITNKTESIYVNDJAEF 600
QY 601 RHDSGYEVHHOKLVFFAEEDVGSNGKAIIGLMVGGVVIATVITLVMLKKQKTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEEDVGSNGKAIIGLMVGGVVIATVITLVMLKKQKTSIHGV 660
QY 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMKN 695
DB 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMKN 695
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RESULT 14
US-08-104-165-1
: Sequence 1. Application US/08104165
: Patent No. 5877015
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: Goate, Alison Mary
: APPLICANT: Mullan, Michael John
: APPLICANT: Chartier-Harlin, Marie-Christine
: APPLICANT: Owen, Michael John
: TITLE OF INVENTION: Test and Model for Alzheimer's Disease
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
```

```

: STREET: 379 Lytton Avenue
: City: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/104,165
: FILING DATE: 21-JAN-1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 9101307.8
: FILING DATE: 21-JAN-1991
: APPLICATION NUMBER: 9118445.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-104-165-1
:
: Query Match 99.5%; Score 3633; DB 2; Length 695;
: Best Local Similarity 99.7%; Pred. No. 6.9e-264;
: Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
:
QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGKLNHMVONGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGKLNHMVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELOITNVVEANQPVITQNMCKRGRKCKTHPREV:PYRCLVG 120
DB 61 TCIDTKEGILQYCEVYPELOITNVVEANQPVITQNMCKRGRKCKTHPREV:PYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSNLDYGMILPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSNLDYGMILPCGIDKFR 180
QY 181 GVEFVCGPLAESNDVSDAEEDSDVWGGACTDYADGSEKVKYVEVAEEVEVAEVEE 240
DB 181 GVEFVCGPLAESNDVSDAEEDSDVWGGADTYADGSEKVKYVEVAEEVEVAEVEE 240
QY 241 EADDEDDDEGVEEAEPEYERATRTTSIAITTTTTSVEEYVVRVPTTAASTPDV 300
DB 241 EADDEDDDEGVEEAEPEYERATRTTSIAITTTTTSVEEYVVRVPTTAASTPDV 300
QY 301 DKYLETPCDENEAHAFQKAKERLFAKIRERMSQVMEWEAEAEQANLPAKAKVQHF 360
DB 301 DKYLETPCDENEAHAFQKAKERLFAKIRERMSQVMEWEAEAEQANLPAKAKVQHF 360
QY 361 QEKVESLFOEANEERQQLVETHMARVPAEMLNDRRLALENYITALQAVPPRSHVFNMLK 420
DB 361 QEKVESLFOEANEERQQLVETHMARVPAEMLNDRRLALENYITALQAVPPRSHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVMVDVDPKAAQIRSOVMTHFARVIERMKNQSLSLLYNPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVMVDVDPKAAQIRSOVMTHFARVIERMKNQSLSLLYNPVA 480
QY 481 EEIOQVEDLLOKEQNSDDVLANNKISEPRISYGNDAKMLSLTETKTVELLPVNSEFSI 540
DB 481 EEIOQVEDLLOKEQNSDDVLANNKISEPRISYGNDAKMLSLTETKTVELLPVNSEFSI 540
:
: 541 DDLOPHWSFGADSVPAENTENEVEPVDARPAADRLTTRPGSLTNIKTEISEVNLDAEF 600
: DB 541 DDLOPHWSFGADSVPAENTENEVEPVDARPAADRLTTRPGSLTNIKTEISEVNLDAEF 600
: QY 601 RHDSGYEVHOKLVFFPAEDVGSNKGAIIGLMVGGVIAIVITLVMKKKQVTSIHGV 660
: DB 601 RHDSGYEVHOKLVFFPAEDVGSNKGAIIGLMVGGVIAIVITLVMKKKQVTSIHGV 660
: QY 661 VEVDAAVTPEERHLSKMGQNGYENPTYKPFQEQMON 695
: DB 661 VEVDAAVTPEERHLSKMGQNGYENPTYKPFQEQMON 695
:
: RESULT 15
: US-08-464-250-1
: Sequence 1. Application US/08/64250
: Patent No. 6107542
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: COATE, Alison Mary
: APPLICANT: MULLAN, Michael John
: APPLICANT: CHARTIER-HARTIN, Marie-Christine
: APPLICANT: OWEN, Michael John
: TITLE OF INVENTION: Test and Model for Alzheimer's Disease
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,250
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/104,165
: FILING DATE: 21-JAN-1992
: APPLICATION NUMBER: 9101307.8
: FILING DATE: 21-JAN-1991
: APPLICATION NUMBER: 9118445.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-464-250-1
:
: Query Match 99.5%; Score 3633; DB 3; Length 695;
: Best Local Similarity 99.7%; Pred. No. 6.9e-264;
: Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
:
QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGKLNHMVONGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGKLNHMVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELOITNVVEANQPVITQNMCKRGRKCKTHPREV:PYRCLVG 120
DB 61 TCIDTKEGILQYCEVYPELOITNVVEANQPVITQNMCKRGRKCKTHPREV:PYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSNLDYGMILPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSNLDYGMILPCGIDKFR 180
QY 181 GVEFVCGPLAESNDVSDAEEDSDVWGGACTDYADGSEKVKYVEVAEEVEVAEVEE 240
DB 181 GVEFVCGPLAESNDVSDAEEDSDVWGGADTYADGSEKVKYVEVAEEVEVAEVEE 240
QY 241 EADDEDDDEGVEEAEPEYERATRTTSIAITTTTTSVEEYVVRVPTTAASTPDV 300
DB 241 EADDEDDDEGVEEAEPEYERATRTTSIAITTTTTSVEEYVVRVPTTAASTPDV 300
QY 301 DKYLETPCDENEAHAFQKAKERLFAKIRERMSQVMEWEAEAEQANLPAKAKVQHF 360
DB 301 DKYLETPCDENEAHAFQKAKERLFAKIRERMSQVMEWEAEAEQANLPAKAKVQHF 360
QY 361 QEKVESLFOEANEERQQLVETHMARVPAEMLNDRRLALENYITALQAVPPRSHVFNMLK 420
DB 361 QEKVESLFOEANEERQQLVETHMARVPAEMLNDRRLALENYITALQAVPPRSHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVMVDVDPKAAQIRSOVMTHFARVIERMKNQSLSLLYNPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVMVDVDPKAAQIRSOVMTHFARVIERMKNQSLSLLYNPVA 480
QY 481 EEIOQVEDLLOKEQNSDDVLANNKISEPRISYGNDAKMLSLTETKTVELLPVNSEFSI 540
DB 481 EEIOQVEDLLOKEQNSDDVLANNKISEPRISYGNDAKMLSLTETKTVELLPVNSEFSI 540

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Db      61  TCIDTKGILQYQOEYFELQITNVFANOPVTIGNCKRGCKOCKTHPEHVITYRCVWG 120
QY      121  EFVSDALLVPCKELHGERMDVCEETHLHWHIVAKETCSKSTNLHDYGMLLPGCIDKFR 180
Db      121  EFVSDALLVPCKELHGERMDVCEETHLHWHIVAKETCSKSTNLHDYGMLLPGCIDKFR 180
QY      181  GVEFVCCPLAESDNVDSADAFEDSDVMWGAIDYVADGSECKVWEVAREVEEVEE 240
Db      181  GVEFVCCPLAESDNVDSADAFEDSDVMWGAIDYVADGSECKVWEVAREVEEVEE 240
QY      241  EADDORDEDDGDEVEEAEPEYEAEIERTTSIATITTTTTSVEFVVRVP:TAASITPAV 300
Db      241  EADDORDEDDGDEVEEAEPEYEAEIERTTSIATITTTTTSVEFVVRVP:TAASITPAV 300
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Search completed: October 2, 2003, 14:03:36
 Job time : 20 secs

GenCore version 5.1.6
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Perfect score: 3651
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Scoring table: RJSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 156212961 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DR seq length: 0
Maximum DR seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3651	100.0	697	9	US-09-794-748-18
5	3651	100.0	697	9	US-09-794-925-18
6	3651	100.0	697	9	US-09-681-442-18
7	3651	100.0	697	11	US-09-869-414-18
8	3651	100.0	697	11	US-09-548-366-18
9	3643	99.8	697	9	US-09-794-927-16
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20	3641	99.7	695	9	US-09-794-748-12
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ALIGNMENTS

RESULT 1

US-09-794-927-18
: Sequence 18, Application US/09794927
: Patent No. US20010016324A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
: TITLE OF INVENTION: USES
: FILE REFERENCE: 28341/6280FG
: CURRENT APPLICATION NUMBER: US/09/794,927
: PRIOR FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-927-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLPLGALLLAAMTARALEVPTDGNAGLAEPOIAAMFCGRLNMMHMYQNGKWDSPGTX 60
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RESULT 2
US-09-795-847-18
: Sequence 18, Application US/09795847
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Van, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: FILE REFERENCE: 28341/6280DE
: CURRENT APPLICATION NUMBER: US/09/795,847
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
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: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patent in Ver. 2.0
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-795-847-18

Query Match 100.0% Score 3651; DB 9; Length 697;
Best Local Similarity 100.0% Pred No. 3 8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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: Sequence 18, Application US/09794743
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Van, Riqiang
```

;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;; TITLE OF INVENTION: USES
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 28341/6280BC
;; CURRENT APPLICATION NUMBER: US/09/794,743
;; CURRENT FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 18
;; LENGTH: 697
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-794-743-18

Query Match 100.0% Score 3651; DB 9; Length 697;
Best Local Similarity 100.0% Pred. No. 3.8e-228; Indels 0; Gaps 0;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;; Sequence 18, Application US/09794748
;; Patent No. US20020037315A1
;; GENERAL INFORMATION:
;; APPLICANT: Gurney, Mark E.
;; APPLICANT: Bienkowski, Michael J.
;; APPLICANT: Heinrikson, Robert L.
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Yan, Riqiang
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A.
;; TITLE OF INVENTION: USES
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 28341/6280JL
;; CURRENT APPLICATION NUMBER: US/09/794,748
;; CURRENT FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 18
;; LENGTH: 697
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-794-748-18

Query Match 100.0% Score 3651; DB 9; Length 697;
Best Local Similarity 100.0% Pred. No. 3.8e-228; Indels 0; Gaps 0;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
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DB 541 DDLQPHSHFGADSVDPANTENEVEPVDARPAADRGLTTPGSGLTNKTKEEISEVNLDAEF 600
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RESULT 5
US-09-794-925-18
; Sequence 18, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEFQIAFMCGRLNMHNVMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEFQIAFMCGRLNMHNVMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGTLQYCOEVPYELQITNVVEANQPVTIONCKRGKCKTHPHVPIYRCLVG 120
DB 61 TCIDTKEGTLQYCOEVPYELQITNVVEANQPVTIONCKRGKCKTHPHVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLQHERMDVCEETHLHWHVAKETSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLQHERMDVCEETHLHWHVAKETSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVGSADAEEDSDVWVGADTDADGSEDKVVEAEVEE 240
DB 181 GVEFVCCPLAESDNVGSADAEEDSDVWVGADTDADGSEDKVVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVRVPTTAASTPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVRVPTTAASTPDVAV 300
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DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVRVPTTAASTPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERMSQVMREWEAEQAQKNLPKADKXAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERMSQVMREWEAEQAQKNLPKADKXAVIQHF 360
QY 361 QKVSLSLQCEAANERQOQVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK 420
DB 361 QKVSLSLQCEAANERQOQVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK 420
QY 421 KYVRAEQDROHTLKHFEHVRWDPKKAQRTSRQVMTHLRVIIYERMNGSLSLLNVPAVA 480
DB 421 KYVRAEQDROHTLKHFEHVRWDPKKAQRTSRQVMTHLRVIIYERMNGSLSLLNVPAVA 480
QY 481 BEIQDEVDLQKQNYSDVLANMISPRISYGNALMPSLSETKTVLLEPVGESFL 540
DB 481 BEIQDEVDLQKQNYSDVLANMISPRISYGNALMPSLSETKTVLLEPVGESFL 540
QY 541 DDLQPHSHFGADSVDPANTENEVEPVDARPAADRGLTTPGSGLTNKTKEEISEVNLDAEF 600
DB 541 DDLQPHSHFGADSVDPANTENEVEPVDARPAADRGLTTPGSGLTNKTKEEISEVNLDAEF 600
QY 601 RHDSGYEVHSHQKLVFFAEVGSNGKAIIGLMVGGVVIATVITVLMKKKQYTSIHNGV 660
DB 601 RHDSGYEVHSHQKLVFFAEVGSNGKAIIGLMVGGVVIATVITVLMKKKQYTSIHNGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 5
US-09-681-442-18
; Sequence 18, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/628JFG
; CURRENT APPLICATION NUMBER: US/09/681,442
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEFQIAFMCGRLNMHNVMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEFQIAFMCGRLNMHNVMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGTLQYCOEVPYELQITNVVEANQPVTIONCKRGKCKTHPHVPIYRCLVG 120
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Db 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONWCKRGKQKTHPHFVPIYPCIVG 120
Qy 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLHDYGMCLPGGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLHDYGMCLPGGIDKFR 180
Qy 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Qy 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTTTTSVEEVRVPTTAASTPDAY 300
Db 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTTTTSVEEVRVPTTAASTPDAY 300
Qy 301 DKYLETPGDENSHAFQKAKERLEAKHREKMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
Db 301 DKYLETPGDENSHAFQKAKERLEAKHREKMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
Qy 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRYIERMNSLSLLYNYPAVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRYIERMNSLSLLYNYPAVA 480
Qy 481 EIQDEVDLLOKEQNYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
Db 481 EIQDEVDLLOKEQNYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
Qy 541 DLQPHWHSFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNKTEEISEVNLDAEF 600
Db 541 DLQPHWHSFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNKTEEISEVNLDAEF 600
Qy 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGSVVIATVITLVMLKKQYTSIRHGV 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGSVVIATVITLVMLKKQYTSIRHGV 660
Qy 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 7

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US-09-869-414-18
: Sequence 18, Application US/09869414
: Publication No. US20030077226A1
: GENERAL INFORMATION:
: APPLICANT: Beinowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
: FILE REFERENCE: 28341/6280M
: CURRENT APPLICATION NUMBER: US/09/869,414
: PRIOR FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-869-414-18
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Query Match 100.0%; Score 3651; DB 11; length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLPGALLLLAANTARALEVPTOGNAGLLAEAPQIAMFCGCLNHHMVONGKWDSPSGTK 60
Db 1 MLPGALLLLAANTARALEVPTOGNAGLLAEAPQIAMFCGCLNHHMVONGKWDSPSGTK 60
Qy 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONWCKRGKQKTHPHFVPIYPCIVG 120
Db 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONWCKRGKQKTHPHFVPIYPCIVG 120
Qy 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLHDYGMCLPGGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLHDYGMCLPGGIDKFR 180
Qy 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Qy 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTTTTSVEEVRVPTTAASTPDAY 300
Db 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTTTTSVEEVRVPTTAASTPDAY 300
Qy 301 DKYLETPGDENSHAFQKAKERLEAKHREKMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
Db 301 DKYLETPGDENSHAFQKAKERLEAKHREKMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
Qy 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRYIERMNSLSLLYNYPAVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRYIERMNSLSLLYNYPAVA 480
Qy 481 EIQDEVDLLOKEQNYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
Db 481 EIQDEVDLLOKEQNYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
Qy 541 DLQPHWHSFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNKTEEISEVNLDAEF 600
Db 541 DLQPHWHSFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNKTEEISEVNLDAEF 600
Qy 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGSVVIATVITLVMLKKQYTSIRHGV 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGSVVIATVITLVMLKKQYTSIRHGV 660
Qy 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 8

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US-09-548-366-18
: Sequence 18, Application US/09548366
: Publication No. US20030104365A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
: FILE REFERENCE: 28341/6280A
: CURRENT APPLICATION NUMBER: US/09/548,366
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
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: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 65
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-348-366-18

Query Match
Best Local Similarity 100.0%; Score 3651; Db 11; Length 697;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLIAEPOIAHFQGRNLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLIAEPOIAHFQGRNLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQIINNYEANOPVTIONWCKRGKCKTHPHFVPIRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQIINNYEANOPVTIONWCKRGKCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTITTESVEEVVVPPTAASTPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTITTESVEEVVVPPTAASTPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEBVRWDPKKAQIRSOVMTHLRVIERMNSQSLLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEBVRWDPKKAQIRSOVMTHLRVIERMNSQSLLYNYPAVA 480
QY 481 BEIQDEVDLLOKEQYSDVLANMISEPRISYGNALMPSLTETKTIVELLVNGEFSL 540
DB 481 BEIQDEVDLLOKEQYSDVLANMISEPRISYGNALMPSLTETKTIVELLVNGEFSL 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKITEISEVNLDAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKITEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEDVGSNGKAIIGLMVGGVVIATVITLVMKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEDVGSNGKAIIGLMVGGVVIATVITLVMKKQYTSIHGV 660
QY 661 VEYDAVTPERHLSKMQQNGYENPTYKFEQMNKK 697
DB 661 VEYDAVTPERHLSKMQQNGYENPTYKFEQMNKK 697

RESULT 9
US-09-794-927-16
: Sequence 16, Application US/09794927
: Patent No. US20010016324A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrikson, Robert L.
: APPLICANT: Parodi, Luis A.
```

QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697

RESULT 10

US-09-795-847-16
; Sequence 16, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-16

Query Match 99.8%; Score 3643; DB 9; Length 697;
Best Local Similarity 99.7%; Pred. No. 1.3e-227;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNONGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHHTVAKETCEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHHTVAKETCEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATEERTTSIATTTTTFSEVEEYVRPTTAASTPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEEATEERTTSIATTTTTFSEVEEYVRPTTAASTPDVAV 300
QY 301 DKYLETPGSDENHAHFQKAKERLEAKHRMSQVWREWEAEAEQAKNLPKADKAVIOHF 360
DB 301 DKYLETPGSDENHAHFQKAKERLEAKHRMSQVWREWEAEAEQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITACAVPPRRHFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITACAVPPRRHFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERNMQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERNMQSLSLYNVPAVA 480

DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERNMQSLSLYNVPAVA 480
QY 481 EEIODFVDELLQKEQNTSDDVLANMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
DB 481 EEIODFVDELLQKEQNTSDDVLANMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLOPWHSEFGADSVPAANTENEPVDPADPAADRLGTLTRPGSGLNINIKTEETSEVNLDAEF 600
DB 541 DDLOPWHSEFGADSVPAANTENEPVDPADPAADRLGTLTRPGSGLNINIKTEETSEVNLDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIIGIMVGGVVIATVITVLMKKQYTSIHGV 660
DB 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIIGIMVGGVVIATVITVLMKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697

RESULT 11

US-09-794-743-16
; Sequence 16, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-16

Query Match 99.8%; Score 3643; DB 9; Length 697;
Best Local Similarity 99.7%; Pred. No. 1.3e-227;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNONGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHHTVAKETCEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHHTVAKETCEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

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QY 241 EADDEDEDEGEVEEAEPEEATERTTISATTTTTTTSVEEVVPTTAASTPDV 300
Db 241 EADDEDEDEGEVEEAEPEEATERTTISATTTTTTTSVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDNEHAHFOKAKERLEAKHREMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDNEHAHFOKAKERLEAKHREMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
Db 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
Db 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
QY 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
Db 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
QY 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDADF 600
Db 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDADF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIGLMVGCVVIATVITVLMKKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIGLMVGCVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEYDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEYDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 12
US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yao, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2834./6280.1
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 05/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 99.8%; Score 3643; DB 9; Length 697;
Best Local Similarity 99.7%; Pred. No. 1,3e-227;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPIDGNAGLLAEPOIAMFCGRLNMHMVQNGKNDSPSGTK 60
Db 1 MLPGLALLLLAAWTAARALEVPIDGNAGLLAEPOIAMFCGRLNMHMVQNGKNDSPSGTK 60
QY 61 TCIDTREGILQYCOEYVPELQITNVYEAQPVTIQNMCKRGRKCKCTHSHFVTPYRCLVG 120
Db 61 TCIDTREGILQYCOEYVPELQITNVYEAQPVTIQNMCKRGRKCKCTHSHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOEHMVCETHLHWHTVAKETCSFKSTNLDHSGYGMLLPCGTDKFR 180
Db 121 EFVSDALLVPDKCKFLHOEHMVCETHLHWHTVAKETCSFKSTNLDHSGYGMLLPCGTDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYAGSSEDKVVEVAEEAEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYAGSSEDKVVEVAEEAEVEE 240
QY 241 EADDEDEDEGEVEEAEPEEATERTTISATTTTTTTSVEEVVPTTAASTPDV 300
Db 241 EADDEDEDEGEVEEAEPEEATERTTISATTTTTTTSVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDNEHAHFOKAKERLEAKHREMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDNEHAHFOKAKERLEAKHREMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
Db 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
Db 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
QY 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
Db 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTTVELLPVNGEFSL 540
QY 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDADF 600
Db 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVNLDADF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIGLMVGCVVIATVITVLMKKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIGLMVGCVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEYDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEYDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 13
US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yao, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2834./6280H1
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-16

Query Match
Best Local Similarity 99.8%; Score 3643; DB 9; Length 697;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 M L P G L A L L L A A W T A R A L E V P T D G N A G L L A E P Q I A M F C G R L N M H M Y V N G K W S D P S G I K 60
D b 1 M L P G L A L L L A A W T A R A L E V P T D G N A G L L A E P Q I A M F C G R L N M H M Y V N G K W S D P S G I K 60

61 T C I D T K E G I L Q Y C Q E V Y P E L Q I T N V E A N Q P V T I N N C K R G K C K T H P H F V I P Y R C L V G 120
Q y 61 T C I D T K E G I L Q Y C Q E V Y P E L Q I T N V E A N Q P V T I N N C K R G K C K T H P H F V I P Y R C L V G 120
D b 61 T C I D T K E G I L Q Y C Q E V Y P E L Q I T N V E A N Q P V T I N N C K R G K C K T H P H F V I P Y R C L V G 120

121 E F V S D A L L V P D K C K F L H Q E R M D V C E T H L H W H T V A K E T C S E K S I N L H D Y G M L L P C G I D K F R 180
Q y 121 E F V S D A L L V P D K C K F L H Q E R M D V C E T H L H W H T V A K E T C S E K S I N L H D Y G M L L P C G I D K F R 180
D b 121 E F V S D A L L V P D K C K F L H Q E R M D V C E T H L H W H T V A K E T C S E K S I N L H D Y G M L L P C G I D K F R 180

181 G V E F V C C P L A E S D N V S A D A E D D S D V W M G A D T D Y A D G S E D K V V R V A E E E V A E V E E 240
Q y 181 G V E F V C C P L A E S D N V S A D A E D D S D V W M G A D T D Y A D G S E D K V V R V A E E E V A E V E E 240
D b 181 G V E F V C C P L A E S D N V S A D A E D D S D V W M G A D T D Y A D G S E D K V V R V A E E E V A E V E E 240

241 E A D D E D D G D E V E E A E P Y E A T E R T I S A T T I T T T T S E V E E V V R V P T I A A S T P D A V 300
Q y 241 E A D D E D D G D E V E E A E P Y E A T E R T I S A T T I T T T T S E V E E V V R V P T I A A S T P D A V 300
D b 241 E A D D E D D G D E V E E A E P Y E A T E R T I S A T T I T T T T S E V E E V V R V P T I A A S T P D A V 300

301 D K Y L E T P G D E N E H A F O K A K E R L E A K H R E R M S Q V M R E W E E A E R O A K N L P K A D K K A V I Q H F 360
Q y 301 D K Y L E T P G D E N E H A F O K A K E R L E A K H R E R M S Q V M R E W E E A E R O A K N L P K A D K K A V I Q H F 360
D b 301 D K Y L E T P G D E N E H A F O K A K E R L E A K H R E R M S Q V M R E W E E A E R O A K N L P K A D K K A V I Q H F 360

361 Q E K V E S L E Q E A A N E R Q O L V E T H M A R V E A M L N D R R L A L E N Y I T A L Q A V P P R P R H V F N M L K 420
Q y 361 Q E K V E S L E Q E A A N E R Q O L V E T H M A R V E A M L N D R R L A L E N Y I T A L Q A V P P R P R H V F N M L K 420
D b 361 Q E K V E S L E Q E A A N E R Q O L V E T H M A R V E A M L N D R R L A L E N Y I T A L Q A V P P R P R H V F N M L K 420

421 K Y V R A E O K D R O H T L K H F E H R V M V D P K K A A Q I R S O V M T H L R V I Y E R M N O S L S L L Y N V P A V A 480
Q y 421 K Y V R A E O K D R O H T L K H F E H R V M V D P K K A A Q I R S O V M T H L R V I Y E R M N O S L S L L Y N V P A V A 480
D b 421 K Y V R A E O K D R O H T L K H F E H R V M V D P K K A A Q I R S O V M T H L R V I Y E R M N O S L S L L Y N V P A V A 480

481 B E I Q D E V D E L L Q E Q N Y S D D V L A N N I S E P R I S Y G N D A L M P S L T E T K T T V E L L P V N G F S L 540
Q y 481 B E I Q D E V D E L L Q E Q N Y S D D V L A N N I S E P R I S Y G N D A L M P S L T E T K T T V E L L P V N G F S L 540
D b 481 B E I Q D E V D E L L Q E Q N Y S D D V L A N N I S E P R I S Y G N D A L M P S L T E T K T T V E L L P V N G F S L 540

541 D D L Q P W H S F G A D S V P A N T E N E V P D A R P A A D R G L T T R P G S G L T N I K T E E I S E V N L D A E F 600
Q y 541 D D L Q P W H S F G A D S V P A N T E N E V P D A R P A A D R G L T T R P G S G L T N I K T E E I S E V N L D A E F 600
D b 541 D D L Q P W H S F G A D S V P A N T E N E V P D A R P A A D R G L T T R P G S G L T N I K T E E I S E V N L D A E F 600

601 R H D S G Y E V H H O K L V F F A E D V G S N K G A I I G L M V G G V I A T V I V I T L V M L K K K Y T S I H H G V 660
Q y 601 R H D S G Y E V H H O K L V F F A E D V G S N K G A I I G L M V G G V I A T V I V I T L V M L K K K Y T S I H H G V 660
D b 601 R H D S G Y E V H H O K L V F F A E D V G S N K G A I I G L M V G G V I A T V I V I T L V M L K K K Y T S I H H G V 660

661 V E V D A A V T P E E R H L S K M Q Q N G Y E N P T Y K F F E Q M O N K K 697
Q y 661 V E V D A A V T P E E R H L S K M Q Q N G Y E N P T Y K F F E Q M O N K K 697
D b 661 V E V D A A V T P E E R H L S K M Q Q N G Y E N P T Y K F F E Q M O N K K 697

RESULT 14
US-09-681-442-16
; Sequence 16, Application US/09661442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG

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; CURRENT APPLICATION NUMBER: US/09/681.442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-16

Query Match
Best Local Similarity 99.8%; Score 3643; DB 9; Length 697;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 M L P G L A L L L A A W T A R A L E V P T D G N A G L L A E P Q I A M F C G R L N M H M Y V N G K W S D P S G I K 60
Db 1 M L P G L A L L L A A W T A R A L E V P T D G N A G L L A E P Q I A M F C G R L N M H M Y V N G K W S D P S G I K 60

61 T C I D T K E G I L Q Y C Q E V Y P E L Q I T N V E A N Q P V T I N N C K R G K C K T H P H F V I P Y R C L V G 120
Qy 61 T C I D T K E G I L Q Y C Q E V Y P E L Q I T N V E A N Q P V T I N N C K R G K C K T H P H F V I P Y R C L V G 120
Db 61 T C I D T K E G I L Q Y C Q E V Y P E L Q I T N V E A N Q P V T I N N C K R G K C K T H P H F V I P Y R C L V G 120

121 E F V S D A L L V P D K C K F L H Q E R M D V C E T H L H W H T V A K E T C S E K S I N L H D Y G M L L P C G I D K F R 180
Qy 121 E F V S D A L L V P D K C K F L H Q E R M D V C E T H L H W H T V A K E T C S E K S I N L H D Y G M L L P C G I D K F R 180
Db 121 E F V S D A L L V P D K C K F L H Q E R M D V C E T H L H W H T V A K E T C S E K S I N L H D Y G M L L P C G I D K F R 180

181 G V E F V C C P L A E S D N V S A D A E D D S D V W M G A D T D Y A D G S E D K V V R V A E E E V A E V E E 240
Qy 181 G V E F V C C P L A E S D N V S A D A E D D S D V W M G A D T D Y A D G S E D K V V R V A E E E V A E V E E 240
Db 181 G V E F V C C P L A E S D N V S A D A E D D S D V W M G A D T D Y A D G S E D K V V R V A E E E V A E V E E 240

241 E A D D E D D G D E V E E A E P Y E A T E R T I S A T T I T T T T S E V E E V V R V P T I A A S T P D A V 300
Qy 241 E A D D E D D G D E V E E A E P Y E A T E R T I S A T T I T T T T S E V E E V V R V P T I A A S T P D A V 300
Db 241 E A D D E D D G D E V E E A E P Y E A T E R T I S A T T I T T T T S E V E E V V R V P T I A A S T P D A V 300

301 D K Y L E T P G D E N E H A F O K A K E R L E A K H R E R M S Q V M R E W E E A E R O A K N L P K A D K K A V I Q H F 360
Qy 301 D K Y L E T P G D E N E H A F O K A K E R L E A K H R E R M S Q V M R E W E E A E R O A K N L P K A D K K A V I Q H F 360
Db 301 D K Y L E T P G D E N E H A F O K A K E R L E A K H R E R M S Q V M R E W E E A E R O A K N L P K A D K K A V I Q H F 360

361 Q E K V E S L E Q E A A N E R Q O L V E T H M A R V E A M L N D R R L A L E N Y I T A L Q A V P P R P R H V F N M L K 420
Qy 361 Q E K V E S L E Q E A A N E R Q O L V E T H M A R V E A M L N D R R L A L E N Y I T A L Q A V P P R P R H V F N M L K 420
Db 361 Q E K V E S L E Q E A A N E R Q O L V E T H M A R V E A M L N D R R L A L E N Y I T A L Q A V P P R P R H V F N M L K 420

421 K Y V R A E O K D R O H T L K H F E H R V M V D P K K A A Q I R S O V M T H L R V I Y E R M N O S L S L L Y N V P A V A 480
Qy 421 K Y V R A E O K D R O H T L K H F E H R V M V D P K K A A Q I R S O V M T H L R V I Y E R M N O S L S L L Y N V P A V A 480
Db 421 K Y V R A E O K D R O H T L K H F E H R V M V D P K K A A Q I R S O V M T H L R V I Y E R M N O S L S L L Y N V P A V A 480

481 B E I Q D E V D E L L Q E Q N Y S D D V L A N N I S E P R I S Y G N D A L M P S L T E T K T T V E L L P V N G F S L 540
Qy 481 B E I Q D E V D E L L Q E Q N Y S D D V L A N N I S E P R I S Y G N D A L M P S L T E T K T T V E L L P V N G F S L 540
Db 481 B E I Q D E V D E L L Q E Q N Y S D D V L A N N I S E P R I S Y G N D A L M P S L T E T K T T V E L L P V N G F S L 540

541 D D L Q P W H S F G A D S V P A N T E N E V P D A R P A A D R G L T T R P G S G L T N I K T E E I S E V N L D A E F 600
Qy 541 D D L Q P W H S F G A D S V P A N T E N E V P D A R P A A D R G L T T R P G S G L T N I K T E E I S E V N L D A E F 600
Db 541 D D L Q P W H S F G A D S V P A N T E N E V P D A R P A A D R G L T T R P G S G L T N I K T E E I S E V N L D A E F 600

601 R H D S G Y E V H H O K L V F F A E D V G S N K G A I I G L M V G G V I A T V I V I T L V M L K K K Y T S I H H G V 660
Qy 601 R H D S G Y E V H H O K L V F F A E D V G S N K G A I I G L M V G G V I A T V I V I T L V M L K K K Y T S I H H G V 660
Db 601 R H D S G Y E V H H O K L V F F A E D V G S N K G A I I G L M V G G V I A T V I V I T L V M L K K K Y T S I H H G V 660

661 V E V D A A V T P E E R H L S K M Q Q N G Y E N P T Y K F F E Q M O N K K 697
Qy 661 V E V D A A V T P E E R H L S K M Q Q N G Y E N P T Y K F F E Q M O N K K 697
Db 661 V E V D A A V T P E E R H L S K M Q Q N G Y E N P T Y K F F E Q M O N K K 697

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RESULT 15
US-09-869-414-16
: Sequence 16, Application US/09869414
: Publication No. US2003007226A
: GENERAL INFORMATION:
: APPLICANT: Beinkowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
: FILE REFERENCE: 28341/6280M
: CURRENT APPLICATION NUMBER: US/09/869.414
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: 09/416.901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155.493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404.133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101.594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: patentin Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-869-414-16

Query Match 99.8%; Score 3643; DB 11; Length 697;
Best Local Similarity 99.7%; Pred. No. 1.3e-227;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MLPGLALLLLAANTARALEVPTDGNAGLLARPOIAMFCGRLLNMHNVONGKWDSPSC	60
DB	1	MLPGLALLLLAANTARALEVPTDGNAGLLARPOIAMFCGRLLNMHNVONGKWDSPSC	60
QY	61	TCGDTKEGTLQYCOEYVPELQITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRC	120
DB	61	TCGDTKEGTLQYCOEYVPELQITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRC	120
QY	121	EFVSDALLVPDKCFLLHQERMDVCETHLHWHTVAKETSEKSTNLDYGMLLPGCI	180
DB	121	EFVSDALLVPDKCFLLHQERMDVCETHLHWHTVAKETSEKSTNLDYGMLLPGCI	180
QY	181	GVEFVCCPLAESDNDSDADADDSDVWVGCAPTDFAUGSDKVVVEAEENVAEVE	240
DB	181	GVEFVCCPLAESDNDSDADADDSDVWVGCAPTDFAUGSDKVVVEAEENVAEVE	240
QY	241	EADDDEDDGDRVEEAEPEVEEATERITISITATITTTTSEVEVVRVPTTAA	300
DB	241	EADDDEDDGDRVEEAEPEVEEATERITISITATITTTTSEVEVVRVPTTAA	300
QY	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSOVHREWEAEERAKNLPKADK	360
DB	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSOVHREWEAEERAKNLPKADK	360
QY	361	QERVSLEQEAANERQOLVETHMARVEAMINDRRRLALENYITALCAVPPRPR	420
DB	361	QERVSLEQEAANERQOLVETHMARVEAMINDRRRLALENYITALCAVPPRPR	420
QY	421	KYVRAQOKRQHTLKHFEHVRMVDPKAAQIRSONWTHLRVIYERMNOSJLL	480
DB	421	KYVRAQOKRQHTLKHFEHVRMVDPKAAQIRSONWTHLRVIYERMNOSJLL	480
QY	481	SEQDEVELLOKEQNSDDVLAMNISEPRISGNDALMPSLTETKTIVELLVNG	540
DB	481	SEQDEVELLOKEQNSDDVLAMNISEPRISGNDALMPSLTETKTIVELLVNG	540
QY	541	DDLQPHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEIE	600
DB	541	DDLQPHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEIE	600

QY 601 RHDSGYEVHOKLVFFAEADVGSNKGAIIIGLMVGGVVIATVIVILVMIKKQYTSIHGV 660
DB 601 RHDSGYEVHOKLVFFAEADVGSNKGAIIIGLMVGGVVIATVIVILVMIKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

Search completed: October 2, 2003, 14:18:37
Job time : 41 secs

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <30L>
A:Experimental source: Brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke-
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
EMBO J. 7, 949-957, 1988
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN>
A:Cross-references: GB:M15532; NID:q177957; PIDN:AAAS564.1; PID:q177956
R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.J.; Muel-
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation, and biogenesis of the amyloid A4 pro-
A:Reference number: S02638; MUID:88296437; PMID:2903137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Ne-
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:q28817; PIDN:CAA30042.1; PID:q289612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Dewhitt, P.; Scilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi-
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PC2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:q28720; PIDN:CAA30050.1; PID:q28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:q28816; PIDN:CAA30041.1; PID:q299611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vittek, M.P.; Rasool, C.G.; de Sauvage, F.; Vittek, S.M.; Bartus, R.I.; Boer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A:Reference number: A30320
A:Accession: A30320
A:Molecule type: mRNA
A:Status: not compared with conceptual translation
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajjod-Sulkowska, E.M.; Majocha, K.E.; Marcota, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA

A:Residues: 507-770 <2AI>
A:Cross-references: GB:M18734; NID:q178572; PIDN:AAA51726.1; PID:q178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for resi-
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GCT for resi-
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Massers, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuth
Query Match 98.1%; Score 3582.5; DB 1; Length 770;
Best Local Similarity 89.9%; Pred. No. 7.2e-181;
Matches 692; Conservative 2; Mismatches 1; Indels 75; Gaps 1;
QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEFOJAFMFCORLNHNNHNVONGKWDSPSGTK 60
DB : MLPGLALLLLAAWTAARALEVPTDGNAGLLAEFOJAFMFCORLNHNNHNVONGKWDSPSGTK 60
QY 61 TCIDTCKEGILQYCOEYVPELOITINNVANOPTVIONWCKGRKCKTTHFHFVPIRCLVG 120
DB : TCIDTCKEGILQYCOEYVPELOITINNVANOPTVIONWCKGRKCKTTHFHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLMHTVAKETCEKSTNLDHGYGMLLPCGIDKPR 180
DB : EFVSDALLVPDKCKFLHQRMDVCEHLMHTVAKETCEKSTNLDHGYGMLLPCGIDKPR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMGCGADTDYADGSEDKVVEVAEEVAEEVEE 240
DB : GVEFVCCPLAESDNVDSADAEEDSDVMGCGADTDYADGSEDKVVEVAEEVAEEVEE 240
QY 241 EADDDDEDEGDEVEBEAEPEYEATERITTSIATITTTTTSVEEVEVR ----- 288
DB : EADDDDEDEGDEVEBEAEPEYEATERITTSIATITTTTTSVEEVEVR ----- 288
QY 289 ----- 288
DB : ----- 288
QY 301 RAMISRWYFDVTGKCAPFFYGGCGGNRNFTTEYCNVAVCGSASQLLTKTQEPLARD 360
DB : ---VPTTAASTPDVAYKYLETGCDENEHAFKAKERLEAKHREMSQVYRWEAEARQA 345
QY 289 ---VPTTAASTPDVAYKYLETGCDENEHAFKAKERLEAKHREMSQVYRWEAEARQA 345
DB : ---VPTTAASTPDVAYKYLETGCDENEHAFKAKERLEAKHREMSQVYRWEAEARQA 420
QY 346 KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 405
DB : KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 406 QAVPPPRHVFNMKKYVRAEQKDRQHTLKHFEHVMVDPKKAAQIRSOVYTHLVIYER 465
DB : QAVPPPRHVFNMKKYVRAEQKDRQHTLKHFEHVMVDPKKAAQIRSOVYTHLVIYER 540
QY 466 MNQSLLYNVPVAABEIEODEVDELLQKQNYSDOVLANNISEPRTSYGNDALMPSLTET 525
DB : MNQSLLYNVPVAABEIEODEVDELLQKQNYSDOVLANNISEPRTSYGNDALMPSLTET 600
QY 526 KITVELLPVNGEFLDLOPWFHSFGADSVYPANTENEVEPVDARPAADGLITRPSGLTN 585
DB : KITVELLPVNGEFLDLOPWFHSFGADSVYPANTENEVEPVDARPAADGLITRPSGLTN 660
QY 586 IKTEEISEVNLDAEPFRHDSGYEVHVKLVFFAEYDGSNKGAIIGLMVGGVVIATVIVITL 645
DB : IKTEEISEVNLDAEPFRHDSGYEVHVKLVFFAEYDGSNKGAIIGLMVGGVVIATVIVITL 720
QY 646 VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQCYENPTYKFFEQMON 695
DB : VMLKKKQYTSIHGGVVEVDAAVTPEERHLSKMQQCYENPTYKFFEQMON 770
RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg,
EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein; expression pattern in rat brain
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:q55616; P-DN:CAA3C488.1; PID:q55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2469652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCR>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Beher, D.; Masters, C.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein: binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation: copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potemaska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A>Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>
Query Match 96.9%; Score 3536; DB 2; Length 695;
Best Local Similarity 97.0%; Pred. No. 1.8e-178;
Matches 674; Conservative a; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNMMVQNGKMSDPSGK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNMMVQNGKMSDPSGK 60

Qy 61 TCIDTREGILQYQEVYVPELQINNVVANOPVTQNWCKRGKCKCTHPIVYPCRLVG 120
Db 61 TCIDTREGILQYQEVYVPELQINNVVANOPVTQNWCKRGKCKCTHPIVYPCRLVG 120

Qy 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETCSKSTNLHDYGMILPGCKDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETCSKSTNLHDYGMILPGCKDKFR 180

Qy 181 GVEFVCCPLAESDSDVMMGGADTDYADGSKVVEAEVEEVEEVEE 240
Db 181 GVEFVCCPLAESDSDVMMGGADTDYADGSKVVEAEVEEVEEVEEVEE 240

Qy 241 EADDEDEDDGDEVEEAEPEEETTSIATITTTTSTVESVEEVVPTTAASTPDV 300
Db 241 EADDEDEDDGDEVEEAEPEEETTSIATITTTTSTVESVEEVVPTTAASTPDV 300

Qy 301 DKYLETPTGDENEHAHFKAKERLEAKHRMSQVNRWESAERQAKNLPAKAKVYQHF 360
Db 301 DKYLETPTGDENEHAHFKAKERLEAKHRMSQVNRWESAERQAKNLPAKAKVYQHF 360

Qy 361 QEKVESLEQEAANRQQLVTHMARVAMLNRRRLALENYITALQAVPRPRHVNMLK 420
Db 361 QEKVESLEQEAANRQQLVTHMARVAMLNRRRLALENYITALQAVPRPRHVNMLK 420

Qy 421 KYVRAEQDKRQHTLKHFEHVRMDPKAAQIRSQVMTHLRVIYERNQSSLLLYNPVAV 480
Db 421 KYVRAEQDKRQHTLKHFEHVRMDPKAAQIRSQVMTHLRVIYERNQSSLLLYNPVAV 480

Qy 481 EIIODEVDELLQEKONYSDVLANMISEPRIISYGNALMPSLTETKITVELLPVNGEFS 540
Db 481 EIIODEVDELLQEKONYSDVLANMISEPRIISYGNALMPSLTETKITVELLPVNGEFS 540

Qy 541 DDLQPHWSFGADSVYPANTENEVEVDARPAADRGCTTRPGSGLTNKITEELSEVNLDAEF 600
Db 541 DDLQPHWSFGADSVYPANTENEVEVDARPAADRGCTTRPGSGLTNKITEELSEVNLDAEF 600

Qy 601 RHDSYEVHHQKLVFFAEADVGSNKGAIIGLVGGWVIATVITVLVLMKKKQYTSIHGV 660
Db 601 RHDSYEVHHQKLVFFAEADVGSNKGAIIGLVGGWVIATVITVLVLMKKKQYTSIHGV 660

Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
X:Alternate names: proteinase nexin 1;
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sakaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Ikizumi, R.; Yamada, T.; Yoshikawa, S.; Sakaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A>Status: translated from: GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D0604; NID:q220328; PIDN:BAA01456.1; PID:q220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C:Keywords: alternative splicing; amyloid; transmembrane protein
Query Match 96.2%; Score 3511; DB 2; Length 695;
Best Local Similarity 96.5%; Pred. No. 3.6e-177;
Matches 571; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNMMVQNGKMSDPSGK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNMMVQNGKMSDPSGK 60

Qy 61 TCIDTREGILQYQEVYVPELQINNVVANOPVTQNWCKRGKCKCTHPIVYPCRLVG 120
Db 61 TCIDTREGILQYQEVYVPELQINNVVANOPVTQNWCKRGKCKCTHPIVYPCRLVG 120

Qy 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETCSKSTNLHDYGMILPGCKDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETCSKSTNLHDYGMILPGCKDKFR 180

Qy 181 GVEFVCCPLAESDSDVMMGGADTDYADGSKVVEAEVEEVEEVEE 240
Db 181 GVEFVCCPLAESDSDVMMGGADTDYADGSKVVEAEVEEVEEVEE 240

Qy 241 EADDEDEDDGDEVEEAEPEEETTSIATITTTTSTVESVEEVVPTTAASTPDV 300

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Db 241 EADDDDEDGDEVEEAEPEYFATERITTSITATITTTTSEVEEVRVPTTAATPDVAV 300
QY 301 DKYLETPGDENEHAFQAKERLEAKHRERMSQVREWEAEERQAKNLPKADKKAIVQIEF 360
Db 301 DKYLETPGDENEHAFQAKERLEAKHRERMSQVREWEAEERQAKNLPKADKKAIVQIEF 360
QY 361 QKVESLEQEAANROOQVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420
Db 361 QKVESLEQEAANROOQVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLK 420
QY 421 KYVRAFORDRQHTLKHFEVRMVDPKKAQIRSCVMTHLRYIERMNSLSLLYNVPAVA 480
Db 421 KYVRAFORDRQHTLKHFEVRMVDPKKAQIRSCVMTHLRYIERMNSLSLLYNVPAVA 480
QY 481 REIQDEVDDELLOKEONSDVLANMISPRISYGNALMPSLTERKTIVVELLPVNGEESL 540
Db 481 REIQDEVDDELLOKEONSDVLANMISPRISYGNALMPSLTERKTIVVELLPVNGEESL 540
QY 541 DLOQPAHSGADSVANTENEPVDPARPAADRGILTTPGSGLTNIKTEEISEVNLDAEF 600
Db 541 DLOQPAHSGADSVANTENEPVDPARPAADRGILTTPGSGLTNIKTEEISEVNLDAEF 600
QY 601 RHDSGVEVHHOKLVFFAEDVGSNKGAITGLMVGGVVATVITVLMLKKQYTSIHIGV 660
Db 601 RHDSGVEVHHOKLVFFAEDVGSNKGAITGLMVGGVVATVITVLMLKKQYTSIHIGV 660
QY 661 VEVDAAVTPERRLSKMOONGYENPTYKFFEOMON 695
Db 661 VEVDAAVTPERRLSKMOONGYENPTYKFFEOMON 695

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1993
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
C:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:q263150; PID:q263150; PID:q263150;
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 84.8%; Score 3095; DB 2; Length 747;
Best Local Similarity 80.8%; Pred. No. 2,9e+55;
Matches 59%; Conservative 36; Mismatches 42; Indels 54; Gaps 5;
QY 17 ALEVPTDGNAGLLAEPQIANF-CGRNLNMNMVQNGKWDSDPSGTICIDTKRGLQYCOE 75
Db 15 ALEVLVDGNGGLAEPQIANFVARLNMNMVQNGKWDSDPSGTICIDTKRGLQYCOE 71
QY 76 VYPELOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDDLVPDKCKF 135
Db 72 VYPELOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDDLVPDKCKF 131
QY 136 LQQRMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDN 195
Db 132 LQQRMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDN 195
QY 196 VDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 253
Db 192 VDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 249
QY 254 VEEAEPEYFATERITTSITATITTTTSEVEEVRVPTTAATPDVAV 300
Db 254 VEEAEPEYFATERITTSITATITTTTSEVEEVRVPTTAATPDVAV 300
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Db 250 AEEPEPEYFATERITTSITATITTTTSEVEEVRVVCSEQAETGICRAMISRMYDVT 309
QY 289 -----VPTTAASTPDVADKYLETGPDENEHAFQ 317
Db 310 SKCAQFTYGGCGGNRFESDDYCMVCGSVIPATAASTPDVADKYLENPDENEHDFEL 369
QY 318 KAKEHLEAKHREKMSQVREWEAEERQAKNLPKADKKAIVQIEFQKVESLEQEAANROO 377
Db 370 KAKEHLEKREKMSQVREWEAEERQAKNLPKADKKAIVQIEFQKVESLEQEAANROO 429
QY 378 LVETIMARVAMLNDRLALENYITALQAVPPRPRHVFENMLKKYVRAEOKDQHTLKH 457
Db 430 LVETIMARVAMLNDRLALENYITALQADPPRPRHVFENMLKKYVRAEOKDQHTLKH 489
QY 438 EHVMDVPKKAQIRSCVMTHLRYIERMNSLSLLYNVPAVAEIGDEYDELLOKEQNY 497
Db 490 EHVMDVPKKAQIRSCVMTHLRYIERMNSQSFSLYKVPAAVEIODEVDLPQKEONY 549
QY 498 SDDVLANMISPRISYGNALMPSLTERKTIVVELLPVNGEESLDDLPWHSGFADSVPA 557
Db 550 SDDVLANMISPRISYGNALMPSLTERKTIVVELLPVNGEESLDDLPWHSGFADSVPA 609
QY 556 TENEVEVPDARPAADRGILTTPGSGLTNIKTEEISEVNLDAEFHRSQYEVHHOKLVFFA 617
Db 610 TENEVEVPDARPAADRGILTTPGSGLTNIKTEEISEVNMDSYRHDYAEVHHOKLVFFA 669
QY 618 EDVGSNKGAITGLMVGGVVATVITVLMLKKQYTSIHIGVVEVDAAVTPERHLSKM 677
Db 670 EDVGSNKGAITGLMVGGVVATVITVLMLKKQYTSIHIGVVEVDAAVTPERHLSKM 729
QY 678 QONGYENPTYKFFEOMON 695
Db 730 QONGYENPTYKFFEOMON 747

RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - hum
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J. N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secr
A:Reference number: A32761; MUID:89346754; PMID:2569763
C:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain
C:Keywords: cloning artifact

Query Match 57.7%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 1.7e+103;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;
QY 80 LOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDDLVPDKCKFLHQE 139
Db 80 LOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDDLVPDKCKFLHQE 60
QY 140 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDNVDSA 199
Db 61 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDNVDSA 120
QY 200 DAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 259
Db 121 DAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 180
QY 260 EPEYFATERITTSITATITTTTSEVEEVRVPTTAATPDVAV 300
Db 181 EPEYFATERITTSITATITTTTSEVEEVRVVCSEQAETGICRAMISRMYDVTGKCAPF 240
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QY 289 -----VPTTAASPTDAVKYLS:PGENENHAFQKAKERL 323
Ub 241 FYCGCGGNRRNFDIEYCMVACGSAIPTTAASPTDAVKYLETGDNENHAFQKAKERL 300
QY 324 EAKHREMSQVMREWEAEERQAKNLPAKAKVIAQVQKVS:EESANERKQCLVETRM 383
Db 301 EAKHREMSQVMREWEAEERQAKNLPAKAKVIAQVQKVS:LEGEAANERKQCLVETRM 360
QY 384 ARVEAMLNDRRRLALENYITAIQAQVPRPHFVNMMLKKYVRAQOKROHTLX:FEFIVXAV 443
Db 361 ARVEAMLNDRRRLALENYITAIQAQVPRPHFVNMMLKKYVRAQOKROHTLX:FEFIVXAV 420
QY 444 DPKKAQIRSQVMTHLRV:YERMNQSLSLYNNPVAVAEETQDEV 487
Db 421 DPKKAQIRSQVMTHLRV:YERMNQSLSLYNNPVAVAEETQDEV 464

RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
N:Alternate names: CDEI-binding protein
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A49321; S34644; S40519
R:Spencer, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A:Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ex
A:Reference number: A49321; MUID:93250009; PMID:848527
A:Accession: A49321
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
A:Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169
A:Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P131199)
A:Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R:von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A:Description: The human homologue of the murine CDEI binding protein is an amyloid pre
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <VON>
A:Cross-references: EMBL:222572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R:Wasco, W.; Gurubagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A:Title: Isolation and characterization of AP2P2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94335131; PMID:8220425
A:Accession: S40519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:g450391; PIDN:AAC4170.1; PID:g450392
C:Genetics:
A:Gene: GDB:APLP2; APPL2
A:Cross-references: GDB:139159; OMIM:104776
A:Map position: 11q23-11q25
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <SP>

Query Match 47.28; Score 1725; DB 2; Length 763;
Best Local Similarity 45.94; Pred. No. 2.9e-83;
Matches 369; Conservative 112; Mismatches 170; Indels 136; Gaps 19;

QY 5 LALLLLAAATATARALEV:-----PTDGNAG:---LLAEFQIAFMFCGRLANHNVONGKWDSDP 56
Db 15 LLLLLLGLTAPALALAGYLEALAAAGTGFVAEFOIAFMFCGRKANHNVNTQGRKEPSP 74

QY 57 SGTKTCDTREGILOVCOEYPELQITNVVEANQPTIQNMCKRGKQCKTHPEFVYPR 116
Db 75 TGKSCFTEKEEVLOYCOEYPELQITNVVEANQVSDNMCKRDKCKCS--RFTVTPK 132
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QY 117 CLVGEFSDALLVPCKFLQHOERMDVCETHLRHMTVAKECTCSEKSTNLHDYGMLLPGI 176
Db 233 CLVGEFSDALLVPCKQCFHKERMEVCENHQHMTVVYKEACLITQGMTLYSYGMLLPGV 192
QY 177 DKFRGVFVCCPLABESUNVDSADAEEDSDVMWNGADITDYADSGDKVVEVAEEVAE 236
Db 193 DQFHGFEVCCPQTKLIGSVSKEEEDFE-----EEBEDFEFDYDYKSEFPPTAD 245
QY 237 VEE--EEA--DDEDDDDGDEVSEAEPEY-----EEATEKTSIATTTTTTES 282
Db 246 LEDFTEAAVDEDDCEDEDEGEVEYDROYDYDTFKGDDYNEENPTEPGSDGTMSSKE:THD 305
QY 283 VEEV-----VRRVP 290
Db 356 VKAVCSQFAMTGPCRAVMPRWYFDLSKGCQVRFYVGGCGGNRRNFESEYCMVCKAMIP 365
QY 291 TTAASPTDAVKYLETGDNENHAFQKAKERLEAKHREMSQVMREWEAEERQAKNLPK 350
Db 366 PTPLEPTND-VDVYFPTSADDNEHAFQKAKECLEIRHNRNMRDVKKPMWEAELOAKNLPK 424
QY 352 ADKKAIVIOHFQEKVESLEQFAANERQQLVETIMARVEAMLNDRRRLALENYITAIQAQVPP 410
Db 425 AEROTLIQHFQAMWKALEKAAASEKQQLVETHLARVEAMLNDRRRLALENYITAIQAQVPP 484
QY 411 RPRHVENMLKKYVRAEOKDRQHTLKHFFHVRWDPKAAQIRSQVMTHLRVYERMNQSL 470
Db 485 RPRHTLOALRRYVRAENKRLHTIRHYOHLAVDPEKAAQWKSQVMTHLRVYERMNQSL 544
QY 471 SLLYNPVAVAEIQDEVDELQKEQNSDDVLANNISEPRISYNDALMPFSLTEIKTIVE 530
Db 545 SLLYKVPYVAQEQIEEIDELLQEQR-----ADM-----DQFASISETPPDVR 587
QY 531 LLPVNGEESLDDLOPMHSGFADSVDPANTENEVPEVDARPAADRGTLITRPG-----SGLTN 585
Db 588 ---VSSES-REIPPFHPF--HPPALPENE-----DTPELYHPMKKSGVGEQDGLIG 637
QY 586 IKTEISEVN-LDAEFRHDSGYEVHHQKLVFAEDVGS-----NKGAI 627
Db 638 ABEKVINSKNKVDKNVDETLDV--KEMIFNAERVGLLEERESVGPLREDFSLSSAL 695
QY 628 IGLMYGGVVIATVIITVLMKKQYTSIHGCVVEVDRAVTPEERELSKMOONGYENPTY 687
Db 696 TGLLVIAVIAATVIIVISLMURKQYGTISHGIVEVDPMLTPEERHKNKMHGNYENPTY 755
QY 688 KFEQOMQ 694
Db 756 KYLEOMQ 762

RESULT 8
S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A:Description: Complete nucleotide and deduced amino acid sequence of rat amyloid p
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protei
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type protein
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C;Keywords: alternative splicing

F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match	46.88:	Score 1709:	DB 2:	Length 765:
Best Locs. Similarity	45.94:	Pred. No. 2e-82:		
Matches 361:	Conservative 124:	Mismatches 168:	Indels 134:	Gaps 20:
QY	5	LALSLLAANTARALAEV----	PTDGNAG----	LLAEPOIATMFCGRLNMHMVQNGKWDSDP 56
DB	15	LVLLLLGLTAPAAALAGYIEALAA	NAAGTGFAVAEPOIANFCOKLNMHVNIQTCKWEDP 74	
QY	57	SGIKICIDITKEGIIQYQEVPELOI	TNNVEANOPVTIONCKRGKQCKTHPIFYPR 116	
DB	75	TGTKSCIGTKEEV-QYCOEYPELOI	TNNVEANOPVINDSWCRDKKQCRS--HIVIPFK 132	
QY	117	CLVGFYFSDALLVPCKKFLHOERMD	VCETHLHKTIVAKETCSKSTNLHCYGLLPCGI 176	
DB	133	CLVGFYFSDVLLVPENCOFFHOER	MVECEKHQRMHTVVYKAECLTETGTLIYSGYMLPCGV 192	
QY	177	DKFRGVFVCCPLAE--ESDNVDS	ADAEEDSUSVMWGADTDYA--DGECKWVVEAREEE 233	
DB	193	DQFHCTYVCCPQTKVDSDS	IMSKEEBEEEEE---DEEDYALLKSEFFTEACLDNFT 248	
QY	234	VAEVEEESACDDEDDGCEVEE	EAPFYEE-----ATSTTTSIAITTTTIESVEV 287	
DB	249	EAAADESDDEEEEGEVEED	RDYVYDSFKDDYNENRPTIPSSDGTISDKETADHV 304	
QY	288	R-----		---VP: 291
DB	309	KAVGSEQEANTGPCRAVMPRV	FDLSKGKCYRFIYGGCGGNRNFESEDCYCMVCKTWIPP 366	
QY	292	TAASTPDADVOKLET	PGDENEHAFQAKERLEAKHREMSQVMREAEAECAKNLPKA 351	
DB	369	TPLPDND--VDVYFISAD	NDNEHAFQAKEQLETRHRSMDRVKKEWEEAEGLCAKNLPKA 427	
QY	352	DKKAVIQHFQEKVESLEGE	ANERQQLVETHMARVEAMINDRRRLALENYITAIQAVPPR 411	
DB	428	ERQTLIQHFOAVMAKALEKA	EASEKQQLVETHLARVEAMINDRRRLALENYLAA--QSSPPR 487	
QY	412	PRHYVNMKKYVRAEQDKRQHTL	KHFEBHVMVDPKKAAQ--TSQVMTHLRVLYERMSLSLS 471	
DB	488	PHRTQLALRYVRAENKDR	LHTRHYGHVLAVDPEKAAQMKSQVMTHLV--EERNSLSLS 547	
QY	472	LLYNNYPVAABEIODEVDEL	LQKEQNSYSDVLANMISEPRISYGNDAICMPSLTETKTVEL 531	
DB	548	LLYKVPYVAQELQHEIDEL	QQR-----ADM-----DQVTSISEMPVDVVR-- 589	
QY	532	LPVNGEFLDLDQPMHMSG	ADSVAPANTENEYEPVDARP-----AADRGLTRFGSLTN 585	
DB	590	--VSSEES--EEIPPFHPF--	HPFFSLSENE---DIQPELY#PMKKGSGMAEQNG--GLIG 639	
QY	586	IKTEE:SEVN-LDAFFRHDS	QYVEYHHQKLVPEAFEDVGS-----NKGAI 627	
DB	640	AEEKVINSKMKDENMVID	ETLDV--KEMIFNAERVSGLEEDPDSVGPJREDFSLSSSAL 697	
QY	628	IGLMVGGVVIATVITVLMLK	KQYQTSIRHGVEVDAAVAPEDRHLSKMQCNGYENPTY 687	
DB	698	IGLLVIAVIAIVVISLVML	KRYQGTISHGIVE#PMLTPERHLNKMGNHGYENPTY 757	
QY	668	KFFEQMQ 694		
DB	758	KYLSQM 764		

RESULT 9
A49974

beta-amyloid precursor protein 2 homolog APLP2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A49574
R:Stunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A:Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-

A:Reference number: A4974; MUID:94132029; PMID:8300594
A:Accession: A4974
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-751 <SLU>
A:Cross-references: GB:U1571; NID:g558467; PID:AAA50603.1; PID:g558468
A:Note: sequence extracted from NCBI backbone (NCBIP:144636)
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
P:310-360/Domain: animal Kunitz-type proteinase inhibitor homolog <BP>

Query Match	46.5%	Score 1699;	DB 2;	Length 751;
Best Local Similarity	45.6%	Pred. No. 6.4e-82;		
Matches 361;	Conservative 114;	Mismatches 160;	Indels 156;	Gaps 20;
Qy	5	LALLILIAAWTALRV----	PIDGNAG----	LIAEPOIAMFCGRI,NKHNVNQNGKWDSP 56
Db	15	LLVLLILGLTAPAAALAGYIEA	LAANAGTGFAVAEPOIAMFCGCKI,NKHNVIOTGKWEDP 74	
Qy	57	SGTKICIDTKGILLOYCEVYPEL	QITNVVNAOPVTVQNWCKRGKCKTHPHFVYPR 116	
Db	75	TGTKSCLATKEVLOYCEYIPEI	QITNVNAKOPNIDSWCKRDRCKS--HIVIFPK 132	
Qy	117	CVGFHVSDAIIIVDKCKFLHQR	MDVCETHLHWHTVAKETCSKSTINLHDYGMILPCGI 176	
Db	133	CLVGFHVSDDLVPUNCOQFHC	RMWCEKHXORHILVKEACJTEGLIHYCYMLLPCGV 192	
Qy	177	DKRGVFFVCCPLAF--LSDNV	SADAAEDSDVWVGADTVADGSEDKVVEVAB---E 231	
Db	193	DOFHGTETVCCPQTIVSDTMS	KFEDEEE-----DEDEEDYDLDKSEFTE 243	
Qy	232	EEVAEEVEEAD-DEDEDEGD	DEVEE-----AEPYEEATERTTSIATTT 276	
Db	244	ADLEDTFAADEDEEDEE	EEVDEDDYDDYDFKDDYNEENPFSSEGIS----- 298	
Qy	277	TTTTSVEEV-----		286
Db	299	--DKETVHDVAKVCSQEAMT	GPCRAVPMRYFDLSKGCVCVRFYGCNGNRNPFSEDC 356	
Qy	287	----VRVPTTAASTPDADV	KYLETPGDENSHAFKAKERLAKHPMSOVWREWEA 341	
Db	357	MAVCRAIMPPTPLPND--VD	VTFESADDNCHAFQAKOLEIRHNRMRCKWKEWEA 415	
Qy	342	ERQAKNELRADKAVIQIHQ	FEKVESLEGEANERQQLVETHMARVEAMLNDRRLALENY 401	
Db	416	ELQAKNLKPTERTQILQH	FQAWKALSKRAASEKQQLVETHLARVEAMLNDRRLALENY 475	
Qy	402	ITALQAVPRPHVFMMLKKY	VRABQDKROHTLKHFEHVBMWDPKAAQIRSOVTHLRY 462	
Db	476	LAALOSDPPRPHRILOAL	RRYVRAENKDRLHTIRHYOHVLAVDPEKAAQMSQVMTHLHV 535	
Qy	462	IYERMNOSLILNYPVA	VEIQIEVDLLOKQENYSDOVLANNISEPRISYGNDAIMPS 521	
Db	536	IEERNQSLILKYVPY	YAEIQIEIDELLOQR-----ADM-----DQFTSS 578	
Qy	522	LTEKTYVELLPVNGEF	SLDDLQPMHFSFGADSVPAANTENEVEPVDAPPAADRLTRPGS 581	
Db	579	ISENPVDVRSSESE-EI	PPFPLHP-----PSLSENE-----GSMAEODG- 621	
Qy	582	GLTNIKITEISEVN-L	IAEFHDSGYEHHCKLVFPFADVGS-----N 623	
Db	622	GLIGAEKVINSKKN	DENMYIDETLDV--KEMIFNAERVGGLEEEEPESVGPLRUDFSL 679	
Qy	624	KGAILGLMGVGVVIA	TVITVLMLKKQVTSIHGWEVDDAAVTPTEERHLSKMQONGYE 683	
Db	680	SNALIGLLVIAVIA	TVIVISLVMLRKRRQYCTISHGIVEVDPMLTTEERHLNKMQHGYE 739	
Qy	684	NTYKFFEQMQ 694		
Db	740	NPTYKYLEQM 750		

RESULT 10
A46362

A: Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDD:AAA98722.1; GSPDB:GX00
A: Experimental source: strain Bristol N2; clone C42D8
R: Daigle, I.; Li, C.
P: Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
A: Title: apl-1, a Caenorhabditis elegans gene encoding a protein related to the human: bcl-2
A: Reference number: A49414; MUID:94089766; PMID:8265668
A: Accession: A49414
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 7-686 <DAI>
C: Cross-references: GR:U00240; NID:g416296; PILD:AAC46470.1; PID:g416297
C: Gene: CESP:C42D8.8
A: Map position: X
A: Introns: 22/3; 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 580/3
C: Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protease

Query Match 22.1%; Score 815.5; DB 2; Length 686;
Best Local Similarity 29.1%; Pred. No. 1.5e-35;
Matches 222; Conservative 109; Mismatches 27%; Indels 155; Gaps 22;

QY 1 MLPLGLALHAAAMTARALEVPTDGNAGLAFAPQIAMFCGRLLNHNMMNVQNGKWDSDPSGDK 60
Db :
6 IMIGLLIPILVAIVVAEGSPASCKREKEPIWVFATSCGYNQYMIFEGSKWTDEERYA 64
QY 61 TCDTEKRLGICQEYYPELOITNTVEANOPVTIQMKRKGRKCKOIHFIHFVTPRCVLG 120
Db :
64 TCFSGLDLIKCRKAYFSPNNITNIWEYSHEVSISDMCREGSPCK-WTHSVRPYPHCIDG 122
QY 121 EFYSALLVPCKKFLHQEKMDYCETHLHWGTAKETCSSEKSTIN----LDHYGKLPG 174
Db :
123 EFISEALCPHDCCFSIVNSROCNDOYHKWDGCKCKKKSGKNKMIVRFVAVLEPC 182
QY 175 GDKFRGVFVCCPLAEESDNVDADAEEDSDVMWGADIDYADGSEKRWVASEEEV 234
Db :
183 ALDMFTGVFVCCP---NDOTNKTDVCKTK----- 209
QY 235 AEVEEEEADDDEDEDGEDVEEABEPYEATERISTATITTTTSVEEVVVPTIA 254
Db :
210 ---EDDDDDDDDDAYEDCYSESDEKDS----- 236
QY 295 STPDADVCKYLETCGDENEHAHQFKAKERLEAKKHRSMSQVMREEA-----ERQAKLP 349
Db :
237 -EPSQDPFYKIANNWNHEHDFPKAEWRMDEKHKVKDYKWKENGWGLEITRYNEQKAKD-P 294
QY 350 KADKKAIVQ---HPQEKVSLFOAPANEROOLVETENARVEAMNDPRRLALENYIAL- 405
Db :
295 KGAEKFQSQNARFQKTYSLEEHRKMRKEIEAVHDERVOAMLNEKKRDATHDYEQALA 354
QY 405 -QAVPPRPVRHVNMKKYVRAEQKDQHILKHEHVRMVDPKKAQAQIRSQVMTHLRVIYE 464
Db :
355 THYNKPNKHSVLQSLKAYTRAEDKRDMHTLNRYRHLLKADSKEAAYKPTVTHRLEYIDL 414
QY 465 RMNQSLSLLYNP-----AVA---EEIQDEVDELQEQNYSDDVLANKSEPRISY 513
Db :
415 RINGTLAMLRDFPLEKYVVRPIAVTYKKDYRVESPDISVE---DSELPIIHDFEFK 470
QY 514 GN--DALMPSLT---FTKTIPELLPVNGEFDLDDQPWHSFQADSVPANT---ENEVEP 564
Db :
471 NAKLIDVKAPTITAKPVKETDNAKVLPEASDSPFEADEYVEDDEDQVKKTPOMKKVKV 530
QY 565 VDARP-----AADRLTRPCSGLTNIKTER-----LSEYNLDA 598
Db :
531 VDIKPKEIKVIREKKAPKLVTSVQTDDDDDDSSSTSESEDDEKNIKELRVCJ 550
QY 599 E-----FRHDSGYEVHHQKLVFAEDVSGNKGAALGLMVGGVVIATVITVMLK 649
Db :
591 EPIIDEPASYRHD-----KLIOSEPYERSASSVFPYVLASAMFALCIAREAIT 642
QY 650 KKQYTSIIHGCVWEVDAAVTPPERHLKSMQONGYENTPYKFFE 691
643 NASRRRAMRGFIED-VYTPTEERHVAGMGVNGYENTPYTFD 683

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 10 Seconds

(without alignments)
3277.761 Million cell updates/sec

Title: us-09-806-194-18

Perfect score: 3651

Sequence: 1 MDPGLALLLAATARALEV.....QNCYENPTYKFFEQKNK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3582.5	98.1	770	1 A4_HUMAN	P05067 h amyloid b
2	3582.5	98.1	770	1 A4_MACFA	P35601 m amyloid b
3	3576	97.9	753	1 A4_SAISC	C95241 s amyloid b
4	3527.5	96.6	770	1 A4_PIG	P79357 s amyloid b
5	3514.5	96.3	770	1 A4_CAVPO	Q60495 c amyloid b
6	3485.5	95.5	770	1 A4_MOUSE	P12023 m amyloid b
7	3485.5	95.5	770	1 A4_RAT	P08592 r amyloid b
8	1730	47.4	695	1 APP2_MOUSE	Q06335 mus musculus
9	1725	47.2	763	1 APP2_HUMAN	Q06481 homo sapien
10	1709	46.8	765	1 APP2_RAT	P15943 rattus norv
11	1191	32.6	650	1 APP1_HUMAN	P31693 homo sapien
12	1183	32.4	653	1 APP1_MOUSE	Q03157 mus muscul
13	815.5	22.3	686	1 A4_CAEEL	Q10651 caenorhabdi
14	747.5	20.5	887	1 A4_DROME	P14599 drosophila
15	284	7.8	59	1 A4_BOVIN	Q28053 bos taurus
16	280	7.7	58	1 A4_RABIT	Q28748 oryctolagus
17	280	7.7	58	1 A4_SHEEP	Q28757 ovis aries
18	279	7.6	58	1 A4_CANFA	Q28280 canis famil
19	275	7.5	57	1 A4_URSMA	Q29149 ursus marit
20	185.5	5.1	407	1 IE68_HSVSA	Q01042 herpesvirus
21	185.5	5.1	993	1 SCPL1_MOUSE	Q52209 mus muscul
22	176	4.8	2004	1 MOZ2_HUMAN	Q92794 homo sapien
23	175.5	4.8	802	1 NAB3_YEAST	P88996 saccharomyc
24	174	4.8	579	1 G160_HUMAN	Q48378 homo sapien
25	172.5	4.7	793	1 CALD2_HUMAN	Q05582 homo sapien
26	169.5	4.6	297	1 TRT2_HUMAN	P45379 homo sapien
27	169.5	4.6	1875	1 MLP1_YEAST	Q02455 saccharomyc
28	169	4.6	771	1 CALD2_CHICK	P12957 gallus gall
29	168	4.6	721	1 YCF2_OENPT	P31558 oenothera p
30	167.5	4.6	816	1 YG3A_YEAST	P53278 saccharomyc
31	167	4.6	1240	1 YN3A_YEAST	P33945 saccharomyc
32	166.5	4.6	681	1 MF10_HUMAN	Q00556 homo sapien
33	164	4.5	2017	1 MYSN_DROME	Q09323 drosophila

RESULT 1

ID	A4_HUMAN	STANDARD	PAT	770 AA
AC	P05067	P09000	P78438	Q13764
AC	Q9UCB6	Q9UC58		
D1	13-AUG-1987	(Rel. 05, Created)		
DT	01-NOV-1991	(Rel. 20, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-1) (PN-1) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57) (Amyloid intracellular domain 57) (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain 50) (AID(50)); C31].			
GN	APP OR A4 OR AD1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606			
PI	SEQUENCE FROM N.A. (ISOFORM APP695).			
RP	TISSUE-Brain;			
RC	MEDLINE:87144572; PubMed:2881207;			
RA	Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;			
RA	"The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor".			
PL	Nature 325:733-736(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM APP751).			
RC	TISSUE-Brain;			
RA	MEDLINE:88122639; PubMed:2893289;			
RA	Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;			
RA	"A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors".			
RL	Nature 331:525-527(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM APP695).			
RC	MEDLINE:69128427; PubMed:2783775;			
RA	Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;			
RA	"The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons."			
RL	Nucleic Acids Res. 17:517-522(1989).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM APP770).			
RC	MEDLINE:90236318; PubMed:2110105;			
RA	Yoshikai S.-I., Sakaki H., Boh-Ura K., Furuya H., Sakaki Y.;			
RA	"Genomic organization of the human amyloid beta-protein precursor gene."			

34	163.5	4.5	1976	1 MYHA_HUMAN	P35580 homo sapien
35	162.5	4.5	712	1 NUC1_RAT	P13383 rattus norv
36	162.5	4.5	1325	1 G160_MOUSE	P55937 mus musculu
37	162.5	4.5	1332	1 SPT7_YEAST	P51777 saccharomyc
38	161.5	4.4	1976	1 MYHA_RAT	Q9J10C rattus norv
39	160.5	4.4	1955	1 PUNA_PARUN	O61308 parascaris
40	158	4.3	301	1 TRT2_CHICK	P02642 gallus gall
41	157.5	4.3	1976	1 MYHA_BOVIN	Q27992 bos taurus
42	157	4.3	706	1 NUC1_HUMAN	P19338 homo sapien
43	156.5	4.3	5596	1 MDN1_HUMAN	Q9NU22 homo sapien
44	156	4.3	694	1 NUC1_CHICK	P15771 gallus gall
45	155.5	4.3	747	1 KF35_HUMAN	G15066 homo sapien

ALIGNMENTS

RN Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1597857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=909164;
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE=92389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.P., Schoetz T.E.,
 RA Brownstein M.J., Udén I.B., Toshiyuki S., Carninci P., Kravetz S.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mellaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska J., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:935-945(1988).
 RN [10]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [11]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538723;
 RA La Pauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [12]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.B.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN [14]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [15]
 RP SEQUENCE OF 266-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1986).
 RN [16]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease-inhibitory activity.";
 RL Nature 331:530-532(1986).
 RN [17]
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [18]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [19]
 RP SEQUENCE OF 656-737 FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.";
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [20]
 RP SEQUENCE OF 672-681.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88035004; PubMed=3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Teitelotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [21]
 RP SEQUENCE OF 674-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87120328; PubMed=3810169;
 RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
 RT "Characterization and chromosomal localization of a cDNA encoding
 RT brain amyloid of Alzheimer's disease."

Query Match:	98.1%	Score 3582.5;	DB i:	Locatd: 770;
Best Local Similarity:	89.9%	Pred. No. 4.1e-171;		
Matches 592;	Conservative 2;	Mismatches 1;	Indels 75;	Gaps 1;
QY	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPO:AMFCGRLLNMHNQNGKWDSDPGSTK	60	
DB	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPO:AMFCGRLLNMHNQNGKWDSDPGSTK	60	
QY	61	TCIDTKEGILQCYQEVPELQITNNVEANQPVTTIONCKKRGKCKCKTHPHFVPIRCLVG	120	
DB	61	TCIDTKEGILQCYQEVPELQITNNVEANQPVTTIONCKKRGKCKCKTHPHFVPIRCLVG	120	
QY	121	EFVSDALLVPCKFLHQRMDVCETHLHWITVAKETCSEKSTNLDHSGMLLPGGIDKFR	180	
DB	121	EFVSDALLVPCKFLHQRMDVCETHLHWITVAKETCSEKSTNLDHSGMLLPGGIDKFR	180	
QY	181	GVEFVCCPLAESNDVSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE	240	
DB	181	GVEFVCCPLAESNDVSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE	240	
QY	241	EADDEDEDGDEVEEAEPEYEAETRTTIAITTTTTTTSVEVVR	288	
DB	241	EADDEDEDGDEVEEAEPEYEAETRTTIAITTTTTTTSVEVVR	300	
QY	289	-----	288	
DB	301	RAMISRMYFDVTEGKCAPFFYGGCGGNRNFDTREYCHAVCGSANSLSLKTQEP-LARD	360	
QY	289	--- VPTTAASPDADVKEYLETGPDENEHAFKAKERLEAKHRRMSQVMREWEAEFQA	345	
DB	361	FKVLPITTAASPDADVKEYLETGPDENEHAFKAKERLEAKHRRMSQVMREWEAEFQA	420	
QY	346	KNLPKADKAVIQHFOEKVESLEQFAANFRQOLVETHMARVEAMLDNRRLALENYTAL	405	
DB	421	KNLPKADKAVIQHFOEKVESLEQFAANFRQOLVETHMARVEAMLDNRRLALENYTAL	480	
QY	406	QAVPRPRHVNMLKKYVRACQKJROHILK3FHFVRVMDPKKAAQIRSOVMTLKVIVYER	465	
DB	481	QAVPRPRHVNMLKKYVRACQKJROHILK3FHFVRVMDPKKAAQIRSOVMTLKVIVYER	540	
QY	466	MNQSLLLYNPVAAEETQDEVELLQKEQNSDDVLANNI:SEPRISYGNDA:MPSTET	525	
DB	541	MNQSLLLYNPVAAEETQDEVELLQKEQNSDDVLANNI:SEPRISYGNDA:MPSTET	600	
QY	526	KTTVELLPVNGEFSLDDLPWHSGADSVPAANTEVEPVDARPAADRGILTRFGSGJN	585	
DB	601	KTTVELLPVNGEFSLDDLPWHSGADSVPAANTEVEPVDARPAADRGILTRFGSGJN	660	
QY	586	IKTEEISEVNLDARFHDSDGYEVHHOKLVFAEDVGSNKGAIIGLMVGGVVIAIVIVITL	645	
DB	661	IKTEEISEVNLDARFHDSDGYEVHHOKLVFAEDVGSNKGAIIGLMVGGVVIAIVIVITL	720	
QY	646	VMLKKQYITSIHHGVVEVDAAVTEERHLSKMQONGYENPTYKFFEQMGN	695	
DB	721	VMLKKQYITSIHHGVVEVDAAVTEERHLSKMQONGYENPTYKFFEQMGN	770	
RESULT 2				
A4_MACFA				
ID	A4_MACFA	STANDARD:	PRI:	770 AA.
AC	P53601;	Q95KN7;		
DT	01-OCT-1996	(Rel. 34, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease			
DE	amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);			
DE	Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-			
DE	APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);			
DE	Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)			
DE	(Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-			
GN	secretase C-terminal fragment 50); C31].			
APP.				
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;				
Cercopitheinae; Macaca.				
NCBI_TaxID=9541;				
[...]				
SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).				
T:SSUB=Cerebellum;				
MEDLINE=91273117; PubMed=1905108;				
Poditsny M.B., Tolan D.R., Selkoe D.J.;				
"Homology of the amyloid beta protein precursor in monkey and human				
supports a primate model for beta amyloidosis in Alzheimer's				
disease";				
Am. J. Pathol. 138:1423-1435(1991).				
!- FUNCTION: Functions as a cell surface receptor and performs				
physiological functions on the surface of neurons relevant to				
neurite growth, neuronal adhesion and axonogenesis. Involved in				
cell motility and transcription regulation through protein-protein				
interactions (By similarity). Can promote transcription activation				
through binding to APPB1/Tip60 and inhibit Notch signaling through				
interaction with Numb (By similarity). Couples to apoptosis-				
inducing pathways such as those mediated by G(O) and JIP (By				
similarity). Inhibits G(O) alpha ATPase activity (By similarity).				
Acts as a kinesin I membrane receptor, mediating the axonal				
transport of beta-secretase and presenilin 1 (By similarity). May				
be involved in copper homeostasis/oxidative stress through copper				
ion reduction. In vitro, copper-metalated APP induces neuronal				
death directly or is potentiated through Cu(II)-mediated low-				
density lipoprotein oxidation (By similarity). Can regulate				
neurite outgrowth through binding to components of the				
extracellular matrix such as heparin and collagen I and IV (By				
similarity). The splice isoforms that contain the BPTI domain				
possess protease inhibitor activity (By similarity).				
!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators				
with metal-reducing activity. Bind transient metals such as				
copper, zinc and iron (By similarity).				
!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved				
peptides, including C31, are potent enhancers of neuronal				
apoptosis (By similarity).				
!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several				
cytoplasmic proteins, including APPB family members, the APPA				
family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding				
to Dab1 inhibits its serine phosphorylation (By similarity). Also				
interacts with GPCR-like protein Bpp, FPRL1, APPBP1, Ibl, KNS2				
(via its TPR domains) (By similarity). APPBP2 (via BASS) and DOBL				
in vitro, it binds MAPT via the MT-binding domains (By				
similarity). Associates with microtubules in the presence of ATP				
and in a kinesin-dependent manner (By similarity).				
!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface				
protein that rapidly becomes internalized via clathrin-coated				
pits. During maturation, the immature APP (N-glycosylated in the				
endoplasmic reticulum) moves to the Golgi complex where complete				
maturation occurs (O-glycosylated and sulfated). After alpha-				
secretase cleavage, soluble APP is released into the extracellular				
space and the C-terminal is internalized to endosomes and				
lysosomes. Some APP accumulates in secretory transport vesicles				
leaving the late Golgi compartment and returns to the cell				
surface. GammaCTF(59) peptide is located to both the cytoplasm and				
nuclei of neurons (By similarity).				
!- ALTERNATIVE PRODUCTS:				
Event=Alternative splicing; Named isoforms-2;				
Comment=Additional isoforms seem to exist;				
Name=APP770;				
ISOId=P53601-1; Sequence=Displayed;				
Name=APP695;				
ISOId=P53601-2; Sequence=VSP_000010, VSP_000011;				
!- DOMAIN: The basolateral sorting signal (BASS) is required for				
sorting of membrane proteins to the basolateral surface of				
epithelial cells (By similarity).				
!- DOMAIN: The NPXY sequence motif found in many tyrosine-				
phosphorylated proteins is required for the specific binding of				
the PID domain. However additional amino acids either N- or C-				
terminal to the NPXY motif are often required for complete				

interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/gamma-secretase mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-719 by either caspase-3, -3a or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and O-linked glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: BELONGS TO THE APP FAMILY.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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FEI	CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FEI	CHAIN	721	770	GAMMA-CTF(57) (POTENTIAL).
FEI	CHAIN	714	770	GAMMA-CTF(50) (POTENTIAL).
FEI	CHAIN	740	770	C31 (POTENTIAL).
FEI	DOMAIN	748	699	EXTRACELLULAR (POTENTIAL).
FEI	DOMAIN	700	723	POTENTIAL.
FEI	TRANSMEM	700	723	POTENTIAL.
FEI	DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FEI	DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FEI	DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FEI	DOMAIN	291	341	RPT1/KUNIT2 INHIBITOR.
FEI	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FEI	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FEI	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FEI	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FEI	DOMAIN	230	260	ASP/GIU-RICH (ACIDIC).
FEI	DOMAIN	274	280	POLY-THR.
FEI	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FEI	ACT_SITE	301	302	REACTIVE BCND (BY SIMILARITY).
FEI	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
FEI	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FEI	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
FEI	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
FEI	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FEI	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FEI	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FEI	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FEI	SITE	724	734	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FEI	SITE	739	740	CLEAVAGE (BY CASPASES-3, -6, -8 OR -9) (BY SIMILARITY).
FEI	SITE	757	760	ENDOCYTOSIS SIGNAL.
FEI	SITE	759	762	NPXY MOTIF.

FEI	CHAIN	712	770
FE	CHAIN	714	770
FE	CHAIN	721	770
FE	CHAIN	740	770
FE	CHAIN	748	699
FE	DOMAIN	700	723
FE	TRANSMEM	724	770
FE	DOMAIN	96	110
FE	DOMAIN	181	188
FE	DOMAIN	291	341
FE	DOMAIN	391	423
FE	DOMAIN	491	522
FE	DOMAIN	523	540
FE	DOMAIN	732	751
FE	DOMAIN	230	260
FE	DOMAIN	274	280
FE	SITE	144	144
FE	ACT SITE	301	302
FE	SITE	671	672
FE	SITE	672	673
FE	SITE	687	688
FE	SITE	704	704
FE	SITE	706	706
FE	SITE	711	712
FE	SITE	713	714
FE	SITE	720	721
FE	SITE	724	734
FE	SITE	739	740
FE	SITE	757	760
FE	SITE	759	762

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 or send an email to license@isb-sib.ch).

DR EMBL: S61024; AAD14347.1; ..
 DR HSSP: P05067; IAAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICPTASE.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS06280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neutrone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Amyloid; Alternative splicing.
 FT SIGNAL 1 17
 FT CHAIN 18 751
 FT CHAIN 18 568
 FT CHAIN 18 552
 FT CHAIN 553 751
 FT CHAIN 653 694
 FT CHAIN 653 692
 FT CHAIN 669 751
 FT CHAIN 669 694
 FT CHAIN 669 692
 FT CHAIN 653 751
 FT CHAIN 595 751
 FT CHAIN 702 751
 FT CHAIN 721 751
 FT DOMAIN 18 680
 FT TRANSMEM 68 704
 FT DOMAIN 705 751
 FT DOMAIN 96 110
 FT DOMAIN 181 188
 FT DOMAIN 251 341
 FT DOMAIN 316 344
 FT DOMAIN 363 428
 FT DOMAIN 504 521
 FT DOMAIN 713 732
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 240
 FT ACT_SITE 301 302
 FT SITE 652 653
 FT SITE 653 654
 FT SITE 666 669
 FT SITE 685 685
 FT SITE 687 687
 FT SITE 692 693
 FT SITE 694 695
 FT SITE 695 695

FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY). BASOLATERAL SORTING SIGNAL (BY SIMILARITY). CLEAVAGE (BY CASPASES-3,-6,-8 OR -9) (BY SIMILARITY). ENDOCYTOSIS SIGNAL. NPXY MOTIF. COPPER (BY SIMILARITY).
QY	1	MLPGLALLLA	AWTARA	LEVPIDGNAGLLAPQIAMFGRLNMHMNYONGKWDSPGSK 60
DB	2	MLPGLALLLA	AWTARA	LEVPIDGNAGLLAPQIAMFGRLNMHMNYONGKWDSPGSK 60
QY	61	TCIDTKEGILQY	CEVYPEL	QITNVVEANQVPTTGMCKKCKCKCKTHPHVPIYRCVLG 120
DB	61	TCIDTKEGILQY	CEVYPEL	QITNVVEANQVPTTGMCKKCKCKCKTHPHVPIYRCVLG 120
QY	121	EFVSDALLVP	PKCKFLH	QRMVCEVTHLHWHVAKETCSEKSTNLDHYGMLPGIDKFR 180
DB	121	EFVSDALLVP	PKCKFLH	QRMVCEVTHLHWHVAKETCSEKSTNLDHYGMLPGIDKFR 180
QY	181	GVFVCCPLAE	SDNVSDA	ESDSDSVWGGAUTDYADGSEDKVVEVAEEVAEEVEE 240
DB	181	GVFVCCPLAE	SDNVSDA	ESDSDSVWGGAUTDYADGSEDKVVEVAEEVAEEVEE 240
QY	241	EADDEDEDG	DEVEEAE	EPEYEAETITTSIATITTTTTSVEEVVVR----- 258
DB	241	EADDEDEDG	DEVEEAE	EPEYEAETITTSIATITTTTTSVEEVVVR----- 258
QY	289	-----	-----	-----VPTAASPTDAVDKYL 304
DB	301	RAMISRWYF	DTVEGK	CAFFYGGCGGNRNFTDEEYCMVCGSVIPTTAASPTDAVDKYL 360
QY	305	ETPGDENEH	AFQKAK	ERLEAKHRRMSQVMRENEAEERQAKNLPKADKAVIOHFOEKV 364
DB	361	ETPGDENEH	AFQKAK	ERLEAKHRRMSQVMRENEAEERQAKNLPKADKAVIOHFOEKV 420
QY	365	ESLEGEAAN	EROOLVET	HARVEAMLNDRRLALENYITALQAVPPRRPRHVNMLKKYVR 424
DB	421	ESLEGEAAN	EROOLVET	HARVEAMLNDRRLALENYITALQAVPPRRPRHVNMLKKYVR 480
QY	425	AFQKQKQHT	LKHFHRM	VDPKAAQIRSOVMTHLRVYERMNQSLSLYNPAVAEEIQ 484
DB	481	AEQKQKQHT	LKHFHRM	VDPKAAQIRSOVMTHLRVYERMNQSLSLYNPAVAEEIQ 540
QY	485	DEVDELLO	KEQNSD	SVIANMISEPRISYNDALMPSLTFTKTTVELLPVNGEFSIDDLQ 544
DB	541	DEVDELLO	KEQNSD	SVIANMISEPRISYNDALMPSLTFTKTTVELLPVNGEFSIDDLQ 600
QY	545	PMHSGADS	VPANTEN	EVPEVQCARPAADRGTLTPGSGTLNKTKEEISEVNLDAEERHDS 604
DB	601	PMHSGADS	VPANTEN	EVPEVQCARPAADRGTLTPGSGTLNKTKEEISEVNLDAEERHDS 660
QY	605	GVEVHHQK	LVFFAE	DVGSNKGAIIGLMVGGVVVATVITVIMLKKKQYTSIHGHVVEVD 664
DB	661	GVEVHHQK	LVFFAE	DVGSNKGAIIGLMVGGVVVATVITVIMLKKKQYTSIHGHVVEVD 720
QY	665	AAVTPTEH	RLSKMQO	NGYENPTYKFFEQMON 695
DB	721	AAVTPTEH	RLSKMQO	NGYENPTYKFFEQMON 751

RESULT 4
 A4_PIG
 ID A4_PIG STANDARD; PRT: 770 AA.
 AC P79307; Q29023; Q9TU0;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (APP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(4C);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RS [2]
RC SEQUENCE OF 1-136 FROM N.A.
RP TISSUE=Small intestine;
RA Winteroe A.K., Fredholm M.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RS [3]
RC SEQUENCE OF 667-723 FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G10 and JIP (By
CC similarity). Inhibits G10 alpha Arpase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-retarded APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity).

CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).

CC -!- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPRIP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APPB1, IB1, KNS2
CC (via its TPR domains) (By similarity). APPB2 (via bass) and DBP1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of APP
CC and in a kinesin-dependent manner (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clatherin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and

CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).

CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clatherin-mediated
CC endocytosis (By similarity).

CC -!- PM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC similarity).

CC -!- PM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).

CC -!- PM: N- and O-linked glycosylated (By similarity).

CC -!- PM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).

CC -!- PM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -!- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.

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CC -----

DR EMBL: AB032550; BAA84580.1;
DR EMBL: Z84022; CAB06313.1;
DR EMBL: X56127; CAA39592.1;
DR HSPSP: P05067; IAAIP.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4_extra.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPT1.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPT1; 1.
DR SMART: SM000006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 C83 (BY SIMILARITY).
 FT CHAIN 688 713 A2(42) (BY SIMILARITY).
 FT CHAIN 688 711 A3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59).
 FT CHAIN 712 770 GAMMA-CTF(57).
 FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).
 FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 135 155 COPPER-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 732 751 INTERACTION WITH G(C)-ALPHA (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACTINIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT AC1_SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
 Query Match 96.5%; Score 3527.5; DB 1; Length 770;
 Best Local Similarity 88.2%; Pred. No. 2,26-168;
 Matches 679; Conservative 9; Mismatches 7; Indels 75; Gaps 1;
 QY 1 MLPGLALLLAATLAALEVPDGNAGLLAEPOIAFMFCGRUNMNMVONGKWDSPGSK 60
 DB 1 MLPGLALVLAATLAALEVPDGNAGLLAEPOVAMFCGRUNMNMVONGKWDSPGSK 60
 QY 61 TCIDTKESILQCYEYVPELQITNVVEANQPVTIQWCKRCKCKTTHPVIPYCLWG 120
 DB 61 TCIGTKEGILQCYEYVPELQITNVVEANQPVTIQWCKRCKCKTTHPVIPYCLWG 120
 QY 121 EFVSDALLVPDKCKFLHQRMQVCEETHLHWHVAKETSEKSTNLHDYGMLLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMQVCEETHLHWHVAKETSEKSTNLHDYGMLLPGIDKFR 180
 QY 181 GVEFVCCPLAESDNDVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVAEVEE 240
 DB 181 GVEFVCCPLAESDNDVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVAEVEE 240
 QY 241 EMDCDESDSDGDEVEAEPEYEATERTTSIATITTTTIESVEVVEVCSEQAETGPC 300
 DB 241 EAEDDEDDGDEVEAEPEYEATERTTSIATITTTTIESVEVVEVCSEQAETGPC 300

DB 241 EAEDDEDDGDEVEAEPEYEATERTTSIATITTTTIESVEVVEVCSEQAETGPC 300
 QY 289 -----
 DB 301 RANISRWYFDVTEGKCAPFFYGGCGGNNEFDTEYCHAVCGSYMSSJLKTTOEHLPOD 360
 QY 289 ---VPTIAASTPDADVDKYLETPGDENEHAHFQKAKERLEAKHREHMSQVMREWEAEHQ 345
 DB 361 PVKLPITIAASTPDADVDKYLETPGDENEHAHFQKAKERLEAKHREHMSQVMREWEAEHQ 420
 QY 346 KNLKADKKAVIQHFOEKVESLEQEAANERQOLVETHEMARVEAKLNDKRRRLALENYITAL 405
 DB 421 KNLKADKKAVIQHFOEKVESLEQEAANERQOLVETHEMARVEAKLNDKRRRLALENYITAL 480
 QY 406 QAVPPRPFRHVNMLKKYVRAQCKDRQHTLKHFERHVRVMDPKKAAQIRSQVTHLRVIYER 465
 DB 481 QAVPPRPFRHVNMLKKYVRAQCKDRQHTLKHFERHVRVMDPKKAAQIRSQVTHLRVIYER 540
 QY 466 MNQSLSLYNVPAVAEEIQDEVDLLOKEQYSDVLANMISEPRISYGNDAIMPSLTET 525
 DB 541 MNQSLSLYNVPAVAEEIQDEVDLLOKEQYSDVLANMISEPRISYGNDAIMPSLTET 600
 QY 526 KTVVLLPVNGEFSLDDI-QPHRSFGADSVDPANTEVEPVDARPAADRGITTRPGSLIN 585
 DB 601 KTVVLLPVNGEFSLDDI-QPHRFGVDSVPANTEVEPVDARPAADRGITTRPGSLIN 660
 QY 586 IKTEEISEVNLDAERHDSGVEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVITL 545
 DB 661 IKTEEISEVNMKDAERHDSGVEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVITL 720
 QY 646 VMLKKKQYTSIHGVSVDAAVTPEERHLSKMQQNGYENPYKFFEQMON 695
 DB 721 VMLKKKQYTSIHGVSVDAAVTPEERHLSKMQQNGYENPYKFFEQMON 770
 RESULT 5
 A4_CAVPO STANDARD; PRT: 770 AA.
 ID A4_CAVPO Q60496;
 AC Q60496; Q60496;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog [contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); Ctf-alpha; Ctf-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CX NCBI_TaxId:10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing.";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOB.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Mack C.J.B., Matsubara E., Governale S., Miquel C.,
 RA Mac W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;

RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA Bigl V.;
RT "Guinea-pig primary cell cultures provide a model to study expression
RT and amyloidogenic processing of endogenous amyloid precursor
RT protein.";
RT Neuroscienc 95:243-254(2000);.
RN [4]

RP GAMMA-SECRETASE PROCESSING;
RX MEDLINE=20576391; PubMed=11035007;
RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.;
RI "A novel gamma-secretase assay based on detection of the putative
RT C-terminal fragment-gamma of amyloid beta protein precursor";
RL J. Biol. Chem. 276:481-487(2001);.

CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/lip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC and apolipoproteins E and J in the CSF and to HDL particles in
CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC -!- FUNCTION: Appicaps elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APP3P1, IBL, KNS2
CC (via its TPR domains), APPBP2 (via HaSS) and DDB1 (By similarity).
CC Associates with microtubules in the presence of APP and in a
CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC ApoE3 appears to be the preferred amyloid binding isoform, while
CC the apoE4 isoform-beta-APP40 complex is capable of being
CC transported across the blood-brain barrier.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated pits
CC (By similarity). During maturation, the immature APP (N
CC glycosylated in the endoplasmic reticulum) moves to the Golgi
CC complex where complete maturation occurs (O-glycosylated and
CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC APP is released into the extracellular space and the C-terminal is
CC internalized to endosomes and lysosomes (By similarity). Some APP
CC accumulates in secretory transport vesicles leaving the late Golgi
CC compartment and returns to the cell surface (By similarity). APP
CC sorts to the basolateral surface in epithelial cells (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms-2;
CC Comment-Additional isoforms, missing exons 7,8 and 15, seem to
CC exist. The L-isoforms, missing exon 15, are referred to as
CC appicans;
CC Name=APP770;

CC IsoId=Q60495-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC brain. The longer isoforms containing the BPTI domain are
CC predominantly expressed in peripheral organs such as muscle and
CC liver.
CC -!- INDUCTION: Increased levels during neuronal differentiation.
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells.
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue (By similarity). The NPXY site is also involved in
CC clathrin-mediated endocytosis.
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC Ctf-alpha and Ctf-beta. Subsequent processing of Ctf-alpha by
CC gamma-secretase yields P3 peptides. This is the major secretory
CC pathway and is non-amyloidogenic. Alternatively,
CC presenilin/picatin-mediated gamma-secretase processing of Ctf-
CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC and amyloid-beta 42 (Abeta42), major components of amyloid
CC plaques, and the corresponding cytotoxic C-terminal fragments
CC (CTFs).
CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC apoptosis (By similarity).
CC -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC sulfate to the L-APP isoforms produces the APP proteoglycan core
CC proteins, the appicans (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific (By similarity).
CC Phosphorylation can affect APP processing, neuronal
CC differentiation and interaction with other proteins.
CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X97631; CAA66230.1; -;
CC EMBL: X99198; CAA67589.1; -;
CC HSSP: P05067; IBA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR008154; A4_extra.
CC Pfam: PF00014; Kunitz_BPTI; 1.
CC PRINTS: PD00203; AMYLOIDA4.
CC PRODOM: PD000222; Kunitz_BPTI; 1.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00131; KU; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS0279: BPTL_KUNITZ_2: 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
FT CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).
FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).
FT CHAIN 688 713 P3(42) (BY SIMILARITY).
FT CHAIN 688 711 P3(44) (BY SIMILARITY).
FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
FT CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).
FT CHAIN 740 770 C31 (BY SIMILARITY).

Query Match 96.3%; Score 3514.5; DB 1; Length 770;
Best Local Similarity 87.9%; Pred No. 9.9e-166;
Matches 677; Conservative 8; Mismatches 10; Indels 75; Gaps 1;

QY 1 MLPGLALLLAATTAALAEVPTDGNAGLAEAPQIAFCGRLLNMNMVQNGKWDSPSGIK 60
DQ 1 MLPGLALLLAATTAALAEVPTDGNAGLAEAPQIAFCGRLLNMNMVQNGKWDSPSGIK 60
QY 61 TCIDTKEGILYCOEYVPELQIIVNEANQPVTONWCKRGSKOCKPHFVIEYRGLNG 120
DQ 61 TCIGSGEGILQCOEYVPELQIIVNEANQPVTONWCKRGSKOCKPHFVIEYRGLNG 120
QY 121 EYVSQALLVPDKCKFLHQRMDVCEETHLHWITVAKETCSKSTINLHDYGMILPGIDKFR 180
DQ 121 EYVSQALLVPDKCKFLHQRMDVCEETHLHWITVAKETCSKSTINLHDYGMILPGIDKFR 180
QY 181 GVEFVCCPLAEISDNDVSDADSDVWNGADTDYADGSDKVKVVAEVEEVAEVEE 240
DQ 181 GVEFVCCPLAEISDNDVSDADSDVWNGADTDYADGSDKVKVVAEVEEVAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEYEATERTTATTTTTTSTESVEEVR----- 288
DQ 241 EADDDEDDGDEVEEAEPEYEATERTTATTTTTTSTESVEEVR----- 288
QY 289 ----- 288
DQ 289 ----- 288
QY 301 RSMISRWYEDVTGKCAPFFYGGCGGNRNFTTEYCMVAGCSVMSONLLKISGEPVSG 360
DQ 301 RSMISRWYEDVTGKCAPFFYGGCGGNRNFTTEYCMVAGCSVMSONLLKISGEPVSG 360
QY 289 ---VPTTAASTPDADVKYLETGDNENAHFOKAKERLEAKHREMSQVMEKEFAGQA 345
DQ 289 ---VPTTAASTPDADVKYLETGDNENAHFOKAKERLEAKHREMSQVMEKEFAGQA 345
QY 361 PVKLPPTAASTPDADVKYLETGDNENAHFOKAKERLEAKHREMSQVMEKEFAGQA 420
DQ 361 PVKLPPTAASTPDADVKYLETGDNENAHFOKAKERLEAKHREMSQVMEKEFAGQA 420
QY 346 KNLPRADKKAVTCHFOEKVESLEQEAANERQOLVETHMARVEMLNDRRIALENYITAL 405
DQ 346 KNLPRADKKAVTCHFOEKVESLEQEAANERQOLVETHMARVEMLNDRRIALENYITAL 405
QY 421 KNLPRADKKAVTCHFOEKVESLEQEAANERQOLVETHMARVEMLNDRRIALENYITAL 460
DQ 421 KNLPRADKKAVTCHFOEKVESLEQEAANERQOLVETHMARVEMLNDRRIALENYITAL 460
QY 405 QAVPPRPRIHVNMLKYYRAEQDKCHTLKPHFHVWVDPKKAQCRSQVWTHLRVIER 465
DQ 405 QAVPPRPRIHVNMLKYYRAEQDKCHTLKPHFHVWVDPKKAQCRSQVWTHLRVIER 465
QY 481 QAVPPRPRIHVNMLKYYRAEQDKCHTLKPHFHVWVDPKKAQCRSQVWTHLRVIER 540
DQ 481 QAVPPRPRIHVNMLKYYRAEQDKCHTLKPHFHVWVDPKKAQCRSQVWTHLRVIER 540
QY 466 MNQSLLLYNPAVAEIQDEYDELLOEQNYSDDV:AMMISEPRISYGNDAIMPSLET 525
DQ 466 MNQSLLLYNPAVAEIQDEYDELLOEQNYSDDV:AMMISEPRISYGNDAIMPSLET 525
QY 541 MNQSLLLYNPAVAEIQDEYDELLOEQNYSDDV:AMMISEPRISYGNDAIMPSLET 600
DQ 541 MNQSLLLYNPAVAEIQDEYDELLOEQNYSDDV:AMMISEPRISYGNDAIMPSLET 600
QY 526 KTTVELLPVNGEFLDQPHWISFGADSVPAANTEVEPEVCPARPAADRLGTRIGSGSLTN 585
DQ 526 KTTVELLPVNGEFLDQPHWISFGADSVPAANTEVEPEVCPARPAADRLGTRIGSGSLTN 585
QY 601 KTTVELLPVNGEFLDQPHWISFGADSVPAANTEVEPEVCPARPAADRLGTRIGSGSLTN 660
DQ 601 KTTVELLPVNGEFLDQPHWISFGADSVPAANTEVEPEVCPARPAADRLGTRIGSGSLTN 660
QY 586 IKTEEISEVNMIAEPRHDSYEVHVKGLVFFAEYDSGSKGALICLWGVVIAIVIVITL 645
DQ 586 IKTEEISEVNMIAEPRHDSYEVHVKGLVFFAEYDSGSKGALICLWGVVIAIVIVITL 645
QY 661 IKTEEISEVNMIAEPRHDSYEVHVKGLVFFAEYDSGSKGALICLWGVVIAIVIVITL 720
DQ 661 IKTEEISEVNMIAEPRHDSYEVHVKGLVFFAEYDSGSKGALICLWGVVIAIVIVITL 720
QY 646 VMLKKKQYTSIHGQVVEVDAVTPERHLNKKMQONGYENPTYKFFEQMQN 695
DQ 646 VMLKKKQYTSIHGQVVEVDAVTPERHLNKKMQONGYENPTYKFFEQMQN 695

Db 721 VMLKKKQYTSIHGQVVEVDAVTPERHLNKKMQONGYENPTYKFFEQMQN 770
RESULT 6
A4_MOUSE STANDARD: PRI: 770 AA.
AC P12023; P97497; P97942; Q99K32;
DT 01-OCT-1989 (Rel. 12; Created)
DT 15-SEP-2003 (Rel. 42; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99;
DE (APP-C99); Beta-amyloid protein 42 (Beta-Ap42); Beta-amyloid protein
DE 40 (Beta-Ap40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE 50) (AID(50)); C31].
GN APP.
OS Mus musculus (Mouse).
CC Fukuyama; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE-Brain;
RC MEDLINE=88106489; PubMed=3322280;
FA Yamada T., Sasaki H., Furuya H., Miyata F., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [2]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=92096458; PubMed=1756177;
FA de Strooper B., van Leuven F., van den Berghe H.;
RT "The amyloid beta protein precursor or proteinase nexin 1 from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN-SAMP8; TISSUE-Hippocampus;
RX PubMed=11235921; PubMed=12477932;
FA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
FA Alvarez J., Morley J.E.;
RT "Molecular cloning, expression, and regulation of hippocampal amyloid
RT precursor protein of senescence accelerated mouse (SAMP8).";
RL Biochem. Cell Biol. 79:57-67(2001).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
FA Izumi R., Yamada T., Yoshikawa S.I., Sasaki H., Hattori M.,
FA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).
RN [6]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC TISSUE-Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
FA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
FA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
FA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
FA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
FA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
FA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
FA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,


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Db 121 EFVSDALLVPCKFLHGRMDVCEETHLHHHTVAKETCSEKSTNLHDYGMLLPGDIFKR 180
Qy 181 GVEFFCCPLAESDNDVSADAEEDSDVWVGADTEYADGSEDKVAVVAFEEVAFVEE 240
Db 182 GVEFFCCPLAESDNDVSADAEEDSDVWVGADTEYADGSEDKVAVVAFEEVAFVEE 240
Qy 241 EADDEDGDEGDEVEEAEPEYBEATRTTSLATTTTTTSTTESVEEVN----- 288
Db 241 EADDEDVDEGDEVEEAEPEYBEATRTTSTATTTTTTSTTESVEEVVAVCSEGAETGPC 320
Qy 289 ----- 298
Db 301 RAKISRWTFDVTESKCVPFYGGGGGGRNNRNFDTSEYCMVCGSVSTQSLKLTSEPFGQ 360
Qy 289 ----VPTTAASPDAVKYLETIPGDNHFAHFKAKERLEAKHRMSQVMKRENEARQA 345
Db 361 PDKLPTTAASPDAVKYLETIPGDNHFAHFKAKERLEAKHRMSQVMKRENEARQA 420
Qy 346 KNLPRADKKAVTQHFQEKVESLEGEANERQCLVETHMARVEAMLNDHRLAENYITAL 400
Db 421 KNLPRADKKAVTQHFQEKVESLEGEANERQCLVETHMARVEAMLNDHRLAENYITAL 480
Qy 406 QAVPRPRHVFNMLKKYVRAEKQKHQHTLKFEHVMVMDPKKAAQIRSQVNIHLRYIER 465
Db 481 QAVPRPRHVFNMLKKYVRAEKQKHQHTLKFEHVMVMDPKKAAQIRSQVNIHLRYIER 540
Qy 466 MNOSSLNLYNPVPAVEETODEVDELLQEQNSYDVIANMTSEPRISYGNVALMPS:TFET 525
Db 541 MNOSSLNLYNPVPAVEETODEVDELLQEQNSYDVIANMTSEPRISYGNVALMPS:TFET 600
Qy 526 KTTVELLPVNGEFLDDLCPSHFCADSVPAANTEVEPEVDARPAADRGLETTPGSGLIN 585
Db 601 KTTVELLPVNGEFLDDLCPSHFCADSVPAANTEVEPEVDARPAADRGLETTPGSGLIN 660
Qy 586 IKTEISEVNLDAEPRHDSGVVHHQKLVFTAEVDGSKNGAIGLIMVGGVVATVIVITL 645
Db 661 IKTEISEVKMDEPQHSDFGFRQKLVFTAEVDGSKNGAIGLIMVGGVVATVIVITL 720
Qy 646 VMLKKKQYTSIHGVVVEYDAVTPPEERHLSKMQNGYENPYKFFEQMON 695
Db 721 VMLKKKQYTSIHGVVVEYDAVTPPEERHLSKMQNGYENPYKFFEQMON 770

RESULT 7
A4_RAT
A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DI 01-AUG-1988 (Rel. 08, Created)
DI 01-DEC-1992 (Rel. 24, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains: Soluble
DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); G31];
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1376(1988).
RX [2]
```

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RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliacopoulos D.,
RA Mytilineou C., Marqolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX PubMed=8996634;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX PubMed=9930726;
RA Katanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.;
RA Suzuki T., Nairn A.C., Greenard P.;
RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
RX PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Gq heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cua Jungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
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DB      685 PTIKYLEQMQ 694
||||| |||||
RESULT 9
APP2_HUMAN
ID APP2_HUMAN STANDARD: PRT: 763 AA.
AC Q06481;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APP2)
DE (CDEI-box binding protein) (CDEBP).
DE APLP2 OR APLP2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93250009; PubMed=8495127;
RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA Morris K., Foster D.C.;
RI "Molecular cloning of the cDNA for a human amyloid precursor protein:
RI homolog: evidence for a multigene family.";
RI Biochemistry 32:4481-4486(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Ranes J., Klaudiny J., Scheit K.H.;
RA "A human amyloid precursor-like protein: is highly homologous to a
RT mouse sequence-specific DNA-binding protein.";
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035131; PubMed=8220435;
RA Wasec W., Gurubhavadatula S., Paralis M., Romano D.M., Sisodia S.S.,
RA Hyman B.I., Neve R.L., Tanzi R.E.;
RI "Isolation and characterization of APLP2 encoding a homologue of the
RI Alzheimer's associated amyloid beta protein precursor.";
RL Nat. Genet. 5:95-99(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISCGEN 3).
RC TISSUE=Lung;
RX MEDLINE=22368257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Gerde J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altshul S.F., Zdobych B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prance C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC MAY BIND TO THE DNA 5'-GTACATG-3' (CDEI BOX).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR

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CC (POENTIAL).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing: Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q06481-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q06481-2; Sequence=VSP_000018;
CC Name=3;
CC IsoId=Q06481-3; Sequence=VSP_000019;
CC -1- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
CC AND ENDOTHELIAL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
CC EMBL: S60099; AAC60589.1; -
CC EMBL: L09209; AAA35526.1; -
CC EMBL: Z22572; CA80295.1; -
CC EMBL: L27631; AAC41701.1; -
CC EMBL: BC000373; AAH00373.1; -
CC PIR: A49321; A49321.
CC ISSP: P05067; IAMP.
CC Genew: HGNC:598; APLP2.
CC MIR: 104776; -
CC GO: GO:0016021; C: integral to membrane; NAS.
CC GO: GO:0005634; C: nucleus; IDA.
CC GO: GO:0003677; F: DNA binding activity; NAS.
CC GO: GO:0007186; P: G-protein coupled receptor protein signaling; NAS.
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR002223; Kunitz_BPTI.
CC Pfam: PF02177; A4_EXTRA; 1.
CC Pfam: PF00314; Kunitz_BPTI; 1.
CC PR: PR:00203; AMYCID4.
CC PR: PR:00759; BASICPTASE.
CC ProDom: PD000222; Kunitz_BPTI; 1.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00133; KC; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE: PS0279; BPTI_KUNITZ_2; 1.
CC Transmembrane: Signal: Alternative splicing; DNA-binding;
CC Nuclear protein; Serine protease inhibitor.
CC SIGNA: 1 29 POTENTIAL.
CC CHAIN 30 763 AMYLOID-LIKE PROTEIN 2.
CC DOMAIN 30 692 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 693 716 POTENTIAL.
CC DOMAIN 717 763 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 225 280 ASP/GLU-RICH (HIGHLY ACIDIC).
CC DOMAIN 306 364 BPTI/KUNITZ INHIBITOR.
CC DOMAIN 215 231 POLY-GLU.
CC ACT_SITE 320 321 REACTIVE BOND (BY SIMILARITY).
CC DISULFID 310 360 BY SIMILARITY.
CC DISULFID 319 343 BY SIMILARITY.
CC DISULFID 335 356 BY SIMILARITY.
CC VARSPIC 308 363 Missing (in isoform 2).
CC VARSPIC 613 624 Missing (in isoform 3).
CC CONFLICT 543 543 /FTid=VSP_000018.
CC SEQUENCE 763 AA; 86955 MW; CA3A7D6DDB8A28D0 CRC64;
CC QUERY MATCH 47.2%; Score 1725; DB 1; Length 763;
CC BEST LOCAL SIMILARITY 46.9%; Pred. No. 8.4e-79;
CC MATCHES 369; Conservative 112; Mismatches 170; Indels 136; Gaps 19;

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QY 5 LALLLLAAWTAALAEV-----PTDGNAS---LLAEPOIAIEFCGKLNHMHVQNGKESDP 56
DB 15 LLLLLLVGLTAPALALAGYIEALAAAGTGFVAFAEPOIAIAFCGKLNHMHVNIQTCKAFPOP 74
QY 57 SGTKTCIDTKEGILQYQOEYVPELOITNVVANGPVTIQWCKRGKQCKTHFEVILPPI 116
DB 75 TGTSKCFETKEVQYQOEYVPELOITNVVANGPVTIQWCKRGKQCKTHFEVILPPI 132
QY 117 CLVGFVSDALLVDPKCKFJLHQRNDVCETHLHWEIVAKFTCTSEKSNJNDHYGMLLPCCI 176
DB 133 CLVGFVSDALLVDPKCKFJLHQRNDVCETHLHWEIVAKFTCTSEKSNJNDHYGMLLPCCI 192
QY 177 DKFRGVFVCCPLAESDNDVSADEEDSDVWNGGADTQYADGSDKDVVEVAEEESVAE 236
DB 193 DFGHGTGVCCPQTKITIGSVKSEEEEDSDVWNGGADTQYADGSDKDVVEVAEEESVAE 245
QY 237 VEE--EEA--DDGDEDDGDEVEEAEDEPY-----DEATERKTSIATITITTES 282
DB 245 LEDFTEAAVDEDEDEECEEVEEDROYVYDTFKGDYNEENPTEPGSDGTMSEKE-THD 305
QY 283 VEEV-----VRVP 290
DB 306 KVAVCSQEMITGPRAVMFRWYFDLSKGCVCVRFYSGCGGNNNFSEDIYCMAYCKAMIP 365
QY 291 TTAASIPDAVQKYLETPGDENPEHAHFOKAKERLEAKHREMSOVNREKEAEKAKNLPK 353
DB 356 TPPLPTND-VDYFETSADDEHARFQAKCELEIRHNRNMDRVKKKEWEAE-CAKNLPK 424
QY 351 ADKKAIVHOFKVBESLECEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPP 410
DB 425 AERQTLIGHFOAVKALEKEAASEKQQLVE-HLARVEAMLNDRRLALENYITALQAVPP 484
QY 411 RPRHVFNLKXVRAEOKDROHTLKHFEHVRWVPKKAQIIRSQVMTHLRVIVERNCSL 470
DB 485 RPRHQLALRVRAENKRLHTIRHYQRLVAVOPFKAAQKQSQVMTHLRVIVERNCSL 544
QY 471 SLLVNPVAAEIOQVDELLQKEQNSDDVLAMNISEPR-SYGNDAIMPLSELTETKTIVE 530
DB 545 SLLVNPVAAEIOQVDELLQKEQNSDDVLAMNISEPR-SYGNDAIMPLSELTETKTIVE 587
QY 531 LLPVNGEFLDQJQWRFSGADSVAPANTENEVEPVDARPAADRLGTLNPG-----SGLTN 585
DB 588 ---VSSEES-EEIPPHFPHF--HPPALPENE-----DIQPELYHPNKKSGVGEODGGLIG 632
QY 586 IKTEGISEVN-LDAEFRGDCGYEVHHCKLVFEADVGS-----NKGAI 627
DB 638 AEKVINKNKVDENKRVITDELTV--KEMIFNAERVGGEIIEERSVGLPREDFSSSSAL 695
QY 628 IGLMVGGVVIATVIVITLVMLKKQYTSIIHGVVEVFAAVTPPEERH-SKMQQNGYENPIY 697
DB 696 IGLLVIAVAIATVIVISLVMLKKQYGTISHGIVEVDPMLTPPEERHLKMQNHGVENPIY 755
QY 688 KFEQOMQ 694
DB 756 KYLEQMQ 762

RESULT 10
APP2_RAT STANDARD; PRT: 765 AA.
AC P15943;
DT 01-APR-1990 (Rel. 14, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid-like protein 2 precursor (Sperm membrane protein YWK-I.).
GN APL22.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxId=10116;
RP SEQUENCE OF 1-627 FROM N.A.
```

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RC STRAIN-Wistar; TISSUE=Brain, and Heart;
RX MEDLINE=94368849; PubMed=8086458;
RA Sandrine R., Masters C.I., Beyreuther K.;
RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
protein precursor-like protein 2 (APLP2/APPH): two amino acids length
difference to human and murine homologues.";
RL Biochim. Biophys. Acta 1219:167-170(1994).
RN [2]
RP SEQUENCE OF 575-765 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=90207205; PubMed=1690887;
RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT "Characterization of cDNA encoding a human sperm membrane protein
related to A4 amyloid protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A;
CC ISOId=P15943-1; Sequence=Displayed;
CC Name=B;
CC ISOId=P15943-2; Sequence=VSP_000021;
CC Name=C;
CC ISOId=P15943-3; Sequence=VSP_00002C;
CC Name=D;
CC ISOId=P15943-4; Sequence=VSP_000020, VSP_000021;
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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or send an email to license@isb-sib.ch).
CC EMBL; X7934; CAA54906.1; -
CC EMBL; M31322; AAA42352.1; -
CC PIR; A35981; A35981.
CC PIR; S42880; S42880.
CC HSP; P05067; IIMP.
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR002223; Kunitz_BPTI.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOID4.
CC PRINTS; PR00759; BASICPTASE.
CC PRODOM; PD000222; Kunitz_BPTI; 1.
CC SMART; SM00131; KU; 1.
CC PROSITE; PS00319; A4_EXTRA; 1.
CC PROSITE; PS00320; A4_INTRA; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS0219; BPTI_KUNITZ_2; 1.
CC Transmembrane: Alternative splicing; Serine protease inhibitor;
KW Signal; Glycoprotein.
KW SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 765 AMYLOID-LIKE PROTEIN 2.
FT DOMAIN 30 695 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 696 718 POTENTIAL.
FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 282 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 308 366 BPTI/KUNITZ INHIBITOR.
FT ACT_SITE 322 323 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 312 362 BY SIMILARITY.
FT DISULFID 321 345 BY SIMILARITY.
FT DISULFID 327 358 BY SIMILARITY.
FT DOMAIN 218 228 POLY-GLU.
FT CARBOHYD 628 629 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT VARSPIC 311 365 Missing (in isoform C and isoform D).
FT VARSPIC 616 627 Missing (in isoform B and isoform D).
```


RA Read J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
 RA Beyer T.A., Multhaup G.,
 RT "Evidence for a copper-binding superfamily of the amyloid precursor
 protein.",
 RL Biochemistry 41:9310-9320(2000).
 CC !- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, A11D1, activates transcription
 CC activation through APB1 (F665) binding (By similarity). Couples
 CC to JIP signal transduction through C-terminal binding. May
 CC interact with cellular G-protein signaling pathways. Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I.
 CC !- FUNCTION: The gamma-CRF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC !- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APB3 and APPA family members,
 CC MARK1P1 and Dab1 (by similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation (By similarity).
 CC !- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC !- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
 CC localized to the postsynaptic density (PSD).
 CC !- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC !- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
 CC similarity).
 CC !- PTM: N-glycosylated.
 CC !- PTM: O-glycosylated.
 CC !- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC
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DR EMBL: 048437; AAB95331.1; ..
 DR EMBL: AD000864; AAB50173.1; ..
 DR EMBL: BC012889; AAB12889.1; ..
 DR HSSP: P05067; 1MMP.
 DR Genew: HGNC:597; APLP1.
 DR MIM: 104775; ..
 DR GO: GO:0005604; C:basement membrane; TAS.
 DR GO: GO:0005208; F:amyloid protein; TAS.
 DR GO: GO:007397; P:histogenesis and organogenesis; TAS.
 DR GO: GO:0007389; P:neurogenesis; TAS.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYIO:DA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 650 AMYLOID-LIKE PROTEIN 1.
 FT CHAIN 62 650 C30 (BY SIMILARITY).
 FT DOMAIN 39 580 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 581 603 POTENTIAL.
 FT DOMAIN 604 650 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 158 178 COPPER-BINDING (BY SIMILARITY).
 FT DOMAIN 204 211 ZINC-BINDING.

FT	DOMAIN	310	342	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	410	441	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	442	459	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	460	643	CLATHRIN-BINDING (POTENTIAL).
FT	DOMAIN	241	247	POLY-GLU.
FT	DOMAIN	264	268	POLY-GLU.
FT	SITE	167	167	REQUIRED FOR COPPER(II) REDUCTION (BY
FT	SITE	604	615	SIMILARITY). SORTING SIGNAL (BY
FT	SITE	620	621	SIMILARITY).
FT	SITE	638	641	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	640	643	ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT	CARBOHYD	337	337	NPXY MOTIF.
FT	CARBOHYD	461	461	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	551	551	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	48	48	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	650 AA:	72176 MW;	A -> P (IN REF. 1).

Query Match 32.6%; Score 1191; DB 1; Length 650;
 Best Local Similarity 38.4%; Pred. No. 2.4e-52;
 Matches 271; Conservative 121; Mismatches 221; Indels 92; Gaps 16;

QY	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNSKWDSPSGTK	60
DB	23	LLPLLLLLLRQAIGSLAGSGAAEAPGSAQVAGLCGRLLTHRDLTGRWEPDQSR	82
QY	61	TCIDTKEGILQYCOEYVPELOIINVEANOPVTIONCKRGKCKTHPHF-VIPEYCLV	119
DB	83	RCRLDPQRVLEYCRQYPELOIARVEQATQAIPIERNCGSGRSGCARPHIQVVFHCLP	142
QY	220	GEFVSDDLVPDKCKFLHQRMDVCETLHWHVTAKETCTSEKSTNLHHDYGMLLPCGDKRF	179
DB	143	GEFVSEALLVPDGGCRFLHQRMDQESSTRHQEQAEACSSQGIILHSGMULLPCGSDRF	202
QY	180	RQVFVCCPLAEESNDSDAEDDDSVWGGADTDYADGSEKDYVEAEVEAEVEE	239
DB	203	REVEYVCCPPPTGTPD--PSGTAVGDPSTRW-----PPGSR---VEGADEE-----EE	246
QY	240	ESADDDEDD--EDGSEVEFEAEPEEATERTISATITTTTIESVEVEVVPVPTASTP	297
DB	247	ESFPQVDDYFVEPPQAEAE--EEVPPSSHTLAVGVKVTPTP-----PT-----	291
QY	296	DAVDKYLETPDGNHSHAFQAKERLEAKHREMSQVMREWEAEARQAKNLPAKDKRAVI	357
DB	292	DCVDITYFGMFGI1SCHEGFLRAKMDLEERMRQINEVMREWAMADNSKNLPKADROALN	351
QY	356	QHFQEKVESLQEAANERQOLVETIMARVEANLDRRLALENVTALQAVPPRRVFN	417
DB	352	EHFQSLQTLREQVSGERQRLVETHTATVIALINDORRAALEGFLAALQADPPQAEVLL	411
QY	418	MLKYVRAEOKDROHILKHFHVRMVDPKAAQIRSQVMTHLRVIYERMNQSLLLYNP	477
DB	412	ALRRYLRAEQEQRHTLRHYQHVAAVDPEKAQMRQFVHTLQVIERVNSGLLLQDNP	471
QY	478	AVAEIQDEYDELLQEQNYSDVLANMISPRISYGNDAIMPSTLTETKITVELLPNGE	537
DB	472	HLAQELRFOIQELHSEH-----LGPSELEA-----PAPGG	502
QY	538	FSLDLQPMHSEFGADSVFANTENEVEPVDARPAADGLTTRPGSGLTNKTETEESEVND	597
DB	503	SSED-----KGGLOPPGSKD--DTPMLPKGSTEQDAASPEKEKNPL	543
QY	598	ASFRH-----DSGYEVHH---QKLVFAEDVGSNKGAIIGLMVGGVVIATVITLVL	648
DB	544	EYERKVNASVPRGPFPHSSEIORDDELAPAGTGVSRVAVSGLLIMGAGGSLVLSMLL	603
QY	649	-KKKYOTSTHHCWVEVDAAVTPEERHLSKMOQNGYENPTYKFEQ	692
DB	604	RRKKPYGAISHGVVEVDPMILTLEEQQLRELQRHGYENPTYRLEE	648

RESULT 12

APPL_MOUSE
ID APPL_MOUSE STANDARD: PRT: 653 AA.
AC Q03157; Q8VC38;
DI 01-OCT-1993 (rel. 27, Created)
DI 01-OCT-1993 (rel. 27, Last sequence update)
DI 15-SEP-2003 (rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30];
GN APLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=93066322; PubMed=1275693;
RA Wasco W., Bupp K., Magendanz M., Guseilia J.F., Tanzi R.E.,
RA Solomon F.,
RA "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10738-10762(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant I.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Garatnac P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay E.J., Hallyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
RN [3]
RP COLLAGEN-BINDING.
RX MEDLINE=9613497; PubMed=8576150;
RA Behr D., Hesse L., Masters C.L., Maltkaup G.,
RA "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1626(1996).
RN [4]
RP INTERACTION WITH DAB1.
RX MEDLINE=9938980C; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheidon M., Curran T.,
RA "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT protein 1.";
RL J. Neurosci. 19:7507-7515(1999).
RN [5]
RP INTERACTION WITH MAPK8IP1.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.,
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [6]
RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
TYR-641.
RX MEDLINE=22313598; PubMed=12228233;
RA Scheinfeld M.H., Gherzi E., Laky K., Fowlkes B.J., D'Adamo L.,
RT Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT secretase regulates transcription.";
RL J. Biol. Chem. 277:44195-44201(2002).
CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, APLP1, activates transcription
CC activation through APBB1 (Fe65) binding. Couples to JIP signal
CC transduction through C-terminal binding. May interact with
CC cellular G-protein signaling pathways. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I.
CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB and APBA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clathrin-mediated
CC endocytosis.
CC -!- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC similarity).
CC -!- PTM: N-glycosylated.
CC -!- PTM: O-glycosylated.
CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: L04538; AAA37247.1;
DR EMBL: BC021877; AAH21877.1;
DR PIR: A46362; A46362.
DR HSSP: P05067; iMWP.
DR KSD: MGI:88046; Aipl.
DR InterPro: IPR001858; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW Glycoprotein.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 553 AMYLOID-LIKE PROTEIN 1.
FT DOMAIN 624 553 C30 (BY SIMILARITY).
FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 606 POTENTIAL.
FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 157 177 COPPER-BINDING.
FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 263 271 POLY-GLU.
FT DOMAIN 535 538 POLY-SER.
FT DOMAIN 601 606 POLY-LEU.
FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
FT SIMILARITY).
FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY


```
Db 6 LMIGLLIPILVA-IYVAEGSPAGSKHKHFI:PMVAFSCUYRQCYM:ILEGSKTKDRIYA 63
QY 61 TCIDTKEGILQVCEWPELOITNNVEANQPVIQNMCKRGGRKQCK:HPHFVIPRCVVG 120
Db 64 TCFSGKLDILKYCRKAYPSMNITNIVEYSISDMCRKEEGSPCK:WTHSVRPYHC:DG 122
QY 121 EFVSALLVPDKCKFLHQBMDVCEIHLHWHFVAKETCSEKSTN:-----LHDYGMLLPC 174
Db 123 EFHSEALQVPHQCQSHVNSRQDCHDYQHWKDFAGKQCK:KSKGNKMKMIVRSFAVLEPC 182
QY 175 GIDKRGVEVFCVPLAEESDNDSDAEDDSVVMWGGADIDYAGSDEKVVVEAEVEEV 234
Db 183 ALDMGTGVFVCCP:-----NDQTKNTDVQKTK:----- 209
QY 235 AEVEEEDADDDEDDGDEVEEAEPEVEATERIT:ATTTTTSVEEVVRVPTTAA 294
Db 210 -----EDDDDDDDAYEDDYSESEKDEE:----- 236
QY 295 STPDVAVDKYLETPGDENEHAHFQKAKLEAKHHRMSQVMREKEA:-----EROAKNLP 349
Db 237 -EPSSODPYFKTANWTHNEHDDFKKEMRMDKHKRKKVQVKMKEWGDLETTRYNEQAKD:P 294
QY 350 KADKKAVIQ:--HFQEKVESLEQEAANEQQVLVETHMARVEAMLNDRRLALENYITAL- 405
Db 295 KGAERFKSOMNARFQKTVSSLEBEHKRMRKEIEAVHEERVQAMLNKKKRDATHQYRQALA 354
QY 406 -QAVPRPRHVFNMKKYVRAEQKDRHTLKHFHEVRMVDPKKAQIRSQVWTH:SVIYE 464
Db 355 THVKNPKNKSIVLOSUKAYIRAEKDRMHTLNRIRHLKADSKRAAYKPTVTHIRURY:DL 414
QY 465 RMNQSLSLLNYP:-----AVA:--EEIQDEVELLQKEQNSDDVILANM:SEPR:SY 513
Db 415 RINGTLAMLRDPDLEKYYRPIANVTYKDYRDVSPDISVE:--DSELPT:HHDEFSK 470
QY 514 GN--DALMPSLT:-----ETKITVELLPVNGEFSLDLQPHWHSFGASVPANT:--ENEVEP 564
Db 471 NAKLDYKAPTITAKPKVETDNKAVLPTEASDEEADYEYEDDQVKKTKPDKKKVKV 530
QY 555 VQARP:-----ADRGLTTRPGSSLTNIKTEE:-----TSVNLDA 598
Db 531 VDIKPKRKVITEERKAPKLVETSVCQTDDEDDDESSSTSESDDEDKK:KELRVSI 590
QY 599 E:-----FRDSEGYEVEHOKLVFFAFQVGSNKGALLGLMVGQVWVATV:VITLVMK 649
Db 591 EPIIDEPASFYRHID:-----KLQSPVEVSASSVFPYVLASAMFITA:CIITAFAT 642
QY 650 KKOYTSIHGHVVEVDAAVTPSEHLSKMOQNOYENKTYKFFE 691
Db 643 NARRRRAMRGFTVD-VYTPPEERHVAGMVGQVNPYTSFED 683
[1]
RESULT 14
A4_DROME: STANDARD: FRT: 867 AA.
AC P14599; Q9TW0; Q9U4H3; Q9W5F1;
CT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Beta-amyloid-like protein precursor.
GN APPL OR VND OR BCNA:GH04413 OR EG:65F1.5 OR CG7727.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=89184650; PubMed=2494667;
RX Rosen D.R., Martin-Morris L., Luo L., White K.;
RA "A Drosophila gene encoding a protein resembling the human
RT beta-amyloid protein precursor."
RL Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN [2]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20194006; PubMed=10731132;
RA Adams M.D., Celiniker S.E., Holt R.A., Evans C.A., Gocayne C.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Attili J.F., Agbayani A., An H.-J., Andrews-Finnkoch C., Baldwin E.,
RA Bailly R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman I.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
RA Nelson D.B., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RC "The genome sequence of Drosophila melanogaster."
RN Science 287:2185-2195(2000).
[3]
REVIEWS.
RC STRAIN=Berkeley;
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celiniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review."
RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[4]
SEQUENCE FROM N.A.
RP STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minina B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valentini P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster."
RN Science 287:2220-2222(2000).
[5]
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ID AA_BOVIN STANDARD; PRT; 59 AA.
AC Q28053.
CT C1-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: beta amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT *Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE G12-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -
DR EMBL: X56126; CAA39591.1; -
DR HSSP: PC5067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutrons; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43465D488A2H12D CRC64;

Query Match 7.8%; Score 284; DB 1; Length 59;
Best Local Similarity 96.6%; Pred. No. 1.5e-06;
Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 591 ISEVNLDAEFRRHDSGYEVHHQKLVFFAEDVGSNKGALIGLVGGVIVATIVTLVMLK 649
Db 1 ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGALIGLVGGVIVATIVTLVMLK 59

Search completed: October 2, 2003, 13:59:39
Job time : 14 secs
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suiua; Suidae; Sus;
OX NCBI_TaxID=9823;

RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RC "Amyloid precursor protein 770,"
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AB03255C; BAA84580.1; -
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 557A1DCB28CC583E CRC64;

Query Match 96.6%; Score 3527.5; DB 6; Length 770;
Best Local Similarity 98.2%; Pred. No. 4.1e-204;
Matches 679; Conservative 9; Mismatches 7; Indels 75; Gaps 1;
QY 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
DB 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIONMCKRCKOCKTHPIVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIONMCKRCKOCKTHPIVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAESDNVSADAEEDSDVWVGADIDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVSADAEEDSDVWVGADIDYADGSEDKVVEAEVEAEVEE 240
QY 241 EADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVVR----- 288
DB 241 EADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVVR----- 288
QY 289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVWREWEAE 345
DB 289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVWREWEAE 345
QY 346 KNLPKADKAVIQHFOEKVESIEQEAANERQOLVETHMARVEAM:NDRRRLALENYIT 405
DB 346 KNLPKADKAVIQHFOEKVESIEQEAANERQOLVETHMARVEAM:NDRRRLALENYIT 405
QY 406 QAVPPRPRHVNMLKKYVRAEQDKROHTLKHFEHVRVMDPKKAQIRSQVMTHLRVIER 465
DB 406 QAVPPRPRHVNMLKKYVRAEQDKROHTLKHFEHVRVMDPKKAQIRSQVMTHLRVIER 465
QY 466 MNQSLSLYNYPVAAEETQDEVELLQKEONYSDVLANMISEPRISYGNALMPSLIT 525
DB 466 MNQSLSLYNYPVAAEETQDEVELLQKEONYSDVLANMISEPRISYGNALMPSLIT 525
QY 541 MNQSLSLYNYPVAAEETQDEVELLQKEONYSDVLANMISEPRISYGNALMPSLIT 600
DB 541 MNQSLSLYNYPVAAEETQDEVELLQKEONYSDVLANMISEPRISYGNALMPSLIT 600
QY 526 KTTVELLPVNGEFLDLDLQPHWFGADSVPAANTENEVEPVDARPAADRGLITRPGSGLN 585

DB 60: KTTVELLPVNGEFLDLDLQPHWFGADSVPAANTENEVEPVDARPAADRGLITRPGSGLN 660
QY 586 IKTEE:SEVNCDAEFRHDSQYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVIAIVITL 645
DB 661 IKTEE:SEVNCDAEFRHDSQYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVIAIVITL 720
QY 646 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 695
DB 721 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 770
RESULTS 4
Q9UGJ8 PRELIMINARY; PRT: 695 AA.
ID Q9UGJ8
AC Q9UGJ8
DI 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms,"
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF289218; AAC00593.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;
Query Match 93.7%; Score 3420; DB 13; Length 695;
Best Local Similarity 93.7%; Pred. No. 1e-197;
Matches 653; Conservative 18; Mismatches 22; Indels 4; Gaps 3;
QY 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
DB 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIONMCKRCKOCKTHPIVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIONMCKRCKOCKTHPIVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAESDNVSADAEEDSDVWVGADIDYADGSEDKVVEAEVEAEVEE 238
DB 181 GVEFVCCPLAESDNVSADAEEDSDVWVGADIDYADGSEDKVVEAEVEAEVEE 240
QY 239 EEEADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVVRVPTTAAS 298
DB 241 EEEADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVVRVPTTAAS 298
QY 299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVWREWEAEQAKNLPKADKAVIQ 358
DB 299 AVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVWREWEAEQAKNLPKADKAVIQ 358
QY 359 HFQEKVESIEQEAANERQOLVETHMARVEAM:NDRRRLALENYIT 418
DB 359 HFQEKVESIEQEAANERQOLVETHMARVEAM:NDRRRLALENYIT 418

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Db 359 HFQKVESLEQFAANERQOLVETHMARVEMLNDHRRIALENYITACCTVPPRPRHVTNM 418
Qy 419 LKKYVRAEQKDRQHTLKHFHVRVYDPKKAQIRSQVMTLKVYIERMNSLSLYNVA 478
Db 419 LKKYVRAEQKDRQHTLKHFHVRVYDPKKAQIRSQVMTLKVYIERMNSLSLYNVA 478
Qy 479 VABEIODEVDELLOKQNYSDVLANMISEPRISYGNALMPSLTETKTYVELLPVNGEF 538
Db 479 VABEIODEVDELLOKQNYSDVLANMISEPRISYGNALMPSLTETKTYVELLPVNGEF 538
Qy 539 SLDDLQPMHSEFAGDSVPANTENEVEPVDARPAADRGILIRPCSGLTNKTKEISEVNLDA 598
Db 539 SLDDLQPMHSEFAGDSVPANTENEVEPVDARPAADRGILIRPCSGLTNKTKEISEVNLDA 598
Qy 599 EFRHDSGYEVHOKLVFFAEDVGSNKGALIGLWGGVVIATVITLVKAKKQYTSIH 658
Db 599 EFRHDSGYEVHOKLVFFAEDVGSNKGALIGLWGGVVIATVITLVKAKKQYTSIH 658
Qy 659 GVVEVDAAVTPERILSKHQQNGYENPTYKFFEQMON 695
Db 659 GVVEVDAAVTPERILSKHQQNGYENPTYKFFEQMON 695

RESULT 5
Q98GJ7 PRELIMINARY: PRT: 751 AA.
AC Q98GJ7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolasse A., Sorribas V.:
RT "Cloning of full-length chicken beta-amyloid precursor protein
isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBS3 databases.
DR EMBL: AC289219; AAC00594.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BP11.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BP2; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPIASE.
DR ProDom: PD000222; Kunitz_BP11; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 92.5%; Score 3379; DB 13; Length 751;
Best Local Similarity 86.6%; Pred. No. 3 4e-195;
Matches 652; Conservative 19; Mismatches 22; Indels 50; Gaps 4;

Qy 1 MFLPCLALLLAAWTARAIEVPTDGNAGLAEPQIAHFCGRNLNMHNVQNGKWDSPGSK 60
Db 1 MLPLALLLLAAGAAALEVADPNAGLAEPQIAHFCGRNLNMHNVQNGKWDSPGSK 60
Qy 61 TCIDTREGILQYCOEYPPQLQTNVVEANQPTIOWCKRGKQCKTPEHVEIYRCLVG 120
Db 61 TCIDTREGILQYCOEYPPQLQTNVVEANQPTIOWCKRGKQCKTPEHVEIYRCLVG 120

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Qy 121 EFVSALLVPDKCKFLHOERMDVCEIHLHWHIVAKETCSEKSTNLHDYGMILPGCIDKFR 180
Db 121 EFVSALLVPDKCKFLHOERMDVCEIHLHWHIVAKETCSEKSTNLHDYGMILPGCIDKFR 180
Qy 181 GYEFVCCPLAESDNDVSDADAEEDSDVWVGADTDYADGSEDKVVE--VAEEVEVAEVE 238
Db 181 GYEFVCCPLAESDNDVSDADAEEDSDVWVGADTDYADGSEDKVVE--VAEEVEVAEVE 238
Qy 239 EEEADDDDEDDGDEVEEAEPEEATERISATITITITTESVEEVEVR----- 288
Db 241 DECADD-DDDDGDEI-BETHEEVEEATERISATITITTESVEEVEVSEQAFTG 258
Qy 289 -----VPTTAATPDPAVK 302
Db 299 PCRAMISRMYPDVAEGKCAPFFYGGCGGNRRNFDEEYCMVCGSVLPTTAASTPDPAVK 358
Qy 303 YLETPGDSNEHAHFOKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKAVIOHFQE 362
Db 359 YLETPGDSNEHAHFOKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKAVIOHFQE 418
Qy 363 KYESLEQSAANERQOLVETHMARVEMLNDRRRLALENYITALOAVPPRPHVNMKKY 422
Db 419 KYESLEQSAANERQOLVETHMARVEMLNDRRRLALENYITALOAVPPRPHVNMKKY 478
Qy 423 VRAEQKDRQHTLKHFHVRVYDPKKAQIRSQVMTLKVYIERMNSLSLYNVAEAE 482
Db 479 VRAEQKDRQHTLKHFHVRVYDPKKAQIRSQVMTLKVYIERMNSLSLYNVAEAE 538
Qy 483 IQHWDELLOKQNYSDVLANMISEPRISYGNALMPSLTETKTYVELLPVNGEFLDD 542
Db 539 IQHWDELLOKQNYSDVLANMISEPRISYGNALMPSLTETKTYVELLPVNGEFLDD 598
Qy 543 LQPMHSEFAGDSVPANTENEVEPVDARPAADRGILIRPCSGLTNKTKEISEVNLDAEFRH 602
Db 599 LQPMHSEFAGDSVPANTENEVEPVDARPAADRGILIRPCSGLTNKTKEISEVNLDAEFRH 658
Qy 603 DSGYEVHOKLVFFAEDVGSNKGALIGLWGGVVIATVITLVKAKKQYTSIHGWE 662
Db 659 DSGYEVHOKLVFFAEDVGSNKGALIGLWGGVVIATVITLVKAKKQYTSIHGWE 718
Qy 663 VDAAVTPERILSKHQQNGYENPTYKFFEQMON 695
Db 719 VDAAVTPERILSKHQQNGYENPTYKFFEQMON 751

RESULT 6
Q98SG0 PRELIMINARY: PRT: 593 AA.
AC Q98SG0
DI 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein A.
DE GN App.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.:
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1; -.
DR HSSP: P05067; LH23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.

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DR PROSITE: PS00319; A4_EXTRA: 1.
DR PROSITE: PS00320; A4_INTRA: 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF658C1AB653 CRC64;

Query Match      87.8%; Score 3206; DB 13; Length 693;
Best Local Similarity 87.5%; Pred. No. 7.9e-185;
Matches 610; Conservative 37; Mismatches 44; Indels 6; Gaps 4;

QY 1 MLPGIALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRINMHMNYONGKWDSPDSGTX 60
DB 1 MLPHITLLVLTG-CALALEVPADGNGLLAEPQIAMFCGKLNHMHMNYONGKWEIDVSGTX 59

QY 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONMCKRGKCKOCTHPHFVPIYRCLVG 120
DB 60 CGICGTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKCKOCTSRTHVVPYRCLVG 119

QY 121 EFVSDALLVPDKCFKFLHQERMDVCETHLHWHYVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 120 EFVSDALLVPDKCFKFLHQERMDICETHLHWHYVAKESKESKMSLSHGYGMLLPGCIDKFR 179

QY 181 GVEFVCCPLAESDNVDSADAEDSDSVWGGADTDYADGSEDKVEVA--EEEFVAVAE 238
DB 180 GVEFVCCPSAESSESFSADSA-EDSDAWGGADADYVDRSDDKRAVEAQPDEEEVEVE 238

QY 239 EEEADDDDEDDGEVEEAEPEEYEEATERTTSIATTTTTSVEEYVVRPTTAASPTD 298
DB 239 EEEADDDDEDDGEVEEAEPEEYEEATERTTSIATTTTTSVEEYVVRVATAASPTD 296

QY 299 AVDKYLETPGDENEHAFQKAKERLEAKHRERMSQVREWEAEACQAKNPKADKAVIQ 358
DB 297 AVDKYLENPNDENEHDFLKAERLECKHREKMSVMEKEEAEQAKNPKADKAVIQ 356

QY 359 HFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRPHVENM 418
DB 357 HFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQADPPRRPHVENM 416

QY 419 LKKYVRAOKDRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVIVERNMQSLSLLYNVPA 478
DB 417 LKKYVRAOKDRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVINERNMQSFLJYKVP 476

QY 479 VAEETQCEVDELLOKEQNYSDVLANNMISEPRISYGNALAKPSLTKTTVELLPVNGE 538
DB 477 VAEETQCEVDELLOKEQNYSDVMNMVSDHRVSYGNALAKPSLTKTTVELLPVNGE 536

QY 539 SLDDQLQPHSFSGADSVDPANTENEVEPVDAARGLTTRPGSGLTNIKTEISEVNLDA 598
DB 537 NIEDQLQPHSFSGVDSVPANTENEVEPVDAARGLTTRPGSGLTNIKTEISEVKNDS 596

QY 599 EFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIH 658
DB 597 EYRHDTAVEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTTIH 656

QY 659 GVEVDDAAVTPPEERHLSKMQONGYENPTYKFEQMON 695
DB 657 GVEVDDAAVTPPEERHLSKMQONGYENPTYKFEQMON 693

RESULT 7
Q98SF9 PRELIMINARY; PRT: 695 AA.
AC Q98SF9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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[1]
KV SEQUENCE FROM N.A.
RP Va: den Hark W.R.;
RI Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298151; CAC37194.1;
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRNTS: PR00203; AMYLOIDA4.
DR SMART: SM00066; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 695 AA; 78603 MW; DC14EB02AFB0204A CRC64;

Query Match      87.2%; Score 3182; DB 13; Length 695;
Best Local Similarity 87.0%; Pred. No. 2.2e-183;
Matches 607; Conservative 40; Mismatches 45; Indels 6; Gaps 5;

QY 1 MLPGIALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRINMHMNYONGKWDSPDSGTX 60
DB 1 MLPHITLLVLTG-CALALEVPADGNGLLAEPQIAMFCGKLNHMHMNYONGKWEIDVSGTX 59

QY 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONMCKRGKCKOCTHPHFVPIYRCLVG 120
DB 60 CGICGTKEGILQYCOEYVPELQITNVVEANQPVTIONMCKRGKCKOCTSRTHVVPYRCLVG 119

QY 121 EFVSDALLVPDKCFKFLHQERMDVCETHLHWHYVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 120 EFVSDALLVPDKCFKFLHQERMDICETHLHWHYVAKESKESKMSLSHGYGMLLPGCIDKFR 179

QY 181 GVEFVCCPLAESDNVDSADAEDSDSVWGGADTDYADGSEDKVEVE--AEDEEVAEVE 238
DB 180 GVEFVCCPSAESSESFSADSA-EDSDVWGGADADYVDRSDDKRAVEAQPDEEEVEVE 238

QY 239 EEEADDDDEDDGEVEEAEPEEYEEATERTTSIATTTTTSVEEYVVR-VPTTAASPT 297
DB 239 EEEADDDDEDDGEVEEAEPEEYEEATERTTSIATTTTTSVEEYVVRVATAVSTP 297

QY 298 AVDKYLETPGDENEHAFQKAKERLEAKHRERMSQVREWEAEQAKN-PKADKAVI 357
DB 298 AVDKYLENPNDENEHDFLKAERLECKHREKMSVMEKEEAEQAKN-PKADKAVI 357

QY 358 HFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRPHVEN 417
DB 358 HFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQADPPRRPHVEN 417

QY 418 MLKKYVRAOKDRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVIVERNMQSLSLLYNVP 477
DB 418 MLKKYVRAOKDRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVINERNMQSFLJYKVP 477

QY 478 AVAEETQCEVDELLOKEQNYSDVLANNMISEPRISYGNALAKPSLTKTTVELLPVNGE 537
DB 478 AVAEETQCEVDELLOKEQNYSDVMNMVSDHRVSYGNALAKPSLTKTTVELLPVNGE 537

QY 538 FSLDDQLQPHSFSGADSVDPANTENEVEPVDAARGLTTRPGSGLTNIKTEISEVNLDA 597
DB 538 FVDEDQLQPHSFSGVDSVPANTENEVEPVDAARGLTTRPGSGLTNIKTEISEVKNMD 597

QY 598 AEFHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIH 657
DB 598 SEYRHDAAYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTTIH 657

QY 658 HGVVEVDDAAVTPPEERHLSKMQONGYENPTYKFEQMON 695
DB 658 HGVVEVDDAAVTPPEERHLSKMQONGYENPTYKFEQMON 695

RESULT 8
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Db 125 VPKRCLVGFVSDALLVFKCKFLHREKMDTCESHLWHTVAKETICGDKIMNLHDYGMLL 184
QY 173 PCGIDKFRGVFVCCPLAESONWDSADAFEDSDSPWNGSNACTDYAGCSHAKVVEVAREE 232
Db 185 PCGIDKFRGVFVCCPIFENDKIDS-DMEEDSDYMGSGDDAAYAGG-DKTV----EF 238
QY 233 EVAEEVEEADDEDEDDEDEVEEE--AEFPYEATEERTTSIATTTITTTESVEEVVAVPT 291
Db 239 KPIEEEEEDESDIDDEDDDD-LDDEVVEDQYEUPTHEITS---STTTTAELEVVVAVPT 295
QY 292 TAASTDPAVDKYLLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERQAKNPKA 351
Db 296 TAASTDPAVDKYLLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERQAKNPKA 355
QY 352 DKAVTQHFQEKVESLEGEAANERQGVETHMARVEAMLNDRRLALENYITALQAVPPR 411
Db 356 DKAVTQHFQEMVESLEGEAASERQGLVETHMARVEAMLNDRRLALENYITALQADPPK 415
QY 412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVMVDPKKAQIRSOVMTHLVIYERMNQSL 471
Db 416 PRHVLNMLKKYSRAEQKDRQHTLKHFEHVMVDPKKAQIRSOVMTHLVIYERMNQSL 475
QY 472 LLYNVPAAVEIQDEVELLQKQNSDDVLANNMISEPRISYGNALMPSLTETKTIVEL 531
Db 476 LLYKVPAAVEIQDEVELLQKQNSDDVLANNMISEPRISYGNALMPSLTETKTIVEL 535
QY 532 LPVNGEESLDDLOPHWSFGADSPANTENEVEPVDPADPAADRGTLTRPGSGLTNKTTEE 591
Db 536 LPDQGEFIDDDLOPHWSPFVIESIPANTENEVEPVDPADPAADRGTLTRPGSGLTNKTTEE 595
QY 592 SEYNLDAEFHDSQGVHVKLVFFAEADVGSNKGAIIGLMVGGVVATVITVLMLKKK 651
Db 596 AELKMETEQDQSGYEVHVKLVFFAEADVGSNKGAIIGLMVGGVVATVITVLMLKKK 655
QY 652 QYTSIHGGVVEVDAVTPERHLSKMQNGYENPTYKFFEQMON 695
Db 656 QYTSIHGGVVEVDAVTPERHLSKMQNGYENPTYKFFEQMON 699

RESULT 10
Q9PVL1 PRELIMINARY; PRT: 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid protein (fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CX NCBI_TaxID:9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Palliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RJ tells us about its function.";
RC Neurochem. Int. 0:0-0 (2003).
DR EMBL: AF030341; AAF12698.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PS00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA: 64753 MW: 0AB8B851863A19D CRC64;

Query Match 75.6%; Score 2759.5; DB 13; Length 569;
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Best Local Similarity 93.2%; Pred. No. 4 6e-158;
Matches 533; Conservative 15; Mismatches 19; Indels 5; Gaps 4;
QY 126 ALLVDPKCKFLHQRMDVCETHLWHTVAKETICSEKSNLHDYGMLLPCGIDKFRGVFV 185
Db 1 ALLVDPKCKLLHQRMDVCETHLWHTVAKESCKSNLHDYGMLLSCGIDKFRGVFV 60
QY 186 CQPLAESDNVDSADAFEDSDVWNGGADTDYAGCSHAKVVE--VAEEVEVAVVEEAD 243
Db 61 CQPLAESDNVDSADAFDDSDVWNGGADYADGSDKVVVEEQEPDEFELTVWDEAD 120
QY 244 DDEDEDGDEVSEEAEEVFEATEKTTSIATTTITTTESVEEVVAVPTTAASTDPAVKY 303
Db 121 DD-DDCGDEI--EETEEVEEATEKTTSIATTTITTTESVEEVVAVPTTAASTDPAVKY 178
QY 304 LETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERQAKNLPKADKKAVIOHFOFK 363
Db 179 LETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERQAKNLPKADKKAVIOHFOFK 238
QY 364 VESLQEAANEKQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKKYV 423
Db 239 VESLQEAANEKQQLVETHMARVEAMLNDRRLALENYITALQVPPRPHVFNMLKKYV 296
QY 424 RAEQKDRQHTLKHFEHVMVDPKKAQIRSOVMTHLVIYERMNQSLSLLYNVPAAVEI 483
Db 299 RAEQKDRQHTLKHFEHVMVDPKKAQIRSOVMTHLVIYERMNQSLSLLYNVPAAVEI 358
QY 484 QDEVDELLOKEQNSDDVLANNMISEPRISYGNALMPSLTETKTIVELLPVNGEESLDD 543
Db 359 QDEVDELLOKEQNSDDVLANNMISEPRISYGNALMPSLTETKTIVELLPVNGEESLDD 418
QY 544 QPHWSFGADSPANTENEVEPVDPADPAADRGTLTRPGSGLTNKTTEEISEYNLDAEFHND 603
Db 419 QPHWSPGVDSVPANTENEVEPVDPADPAADRGTLTRPGSGLTNKTTEEISEYNLDAEFHND 476
QY 604 SGYEVHVKLVFFAEADVGSNKGAIIGLMVGGVVATVITVLMLKKKQYTSIHGGVVEV 663
Db 479 SGYEVHVKLVFFAEADVGSNKGAIIGLMVGGVVATVITVLMLKKKQYTSIHGGVVEV 536

RESULT 11
Q99K32 PRELIMINARY; PRT: 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 68.4 kDa protein (fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC Submitted (MAR-2001) to the EMBL/GenBank/CDDB databases.
DR EMBL: BC005490; AAF05490.1; -.
DR HSSP: P05067; 1AAP.
DR MGD: MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRODom: PD000222; Kunitz_BPTI; 1.
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DR SMARI: SM0013.; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNIT2.1; 1.
DR PROSITE: PS00279; BPTI_KUNIT2.2; 1.
DR Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 58391 MW; BF6802214CBA7C; 172 CRC64;

Query Match 72.0%; Score 2627.5; DB 11; Length 607;
Best Local Similarity 85.3%; Pred. No. 4.4e-150;
Matches 518; Conservative 5; Mismatches 9; Indels 75; Gaps 1;

QY 164 NLHDYGMLLPGCIDKFRGVFVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSED 223
DB 1 NLHDYGMLLPGCIDKFRGVFVCCPLAESDSVDSADAEEDSDVMWGGADIDYADGSED 60
QY 224 KVEVAEEVAEEVAEEADDEDEDEDEVEEEAEFEPEATEERTTSIATITTTTTE 283
DB 61 KVEVAEEVAEEVAEEADDEDEDEVEEEAEFEPEATEERTTSIATITTTTTE 120
QY 284 EFVVR----- 285
DB 121 EEVREVCSOAEITGCRAMISRWFVDTGKVPFFYGGCGGRNNPFDTEEYCMVCGS 180
QY 289 -----VPTTAASTPDADVCKYLETPGDSNEHAHFQKAKERLEAKHR 328
DB 181 VSTOSLLAKTTSEPLPQDPDKLPTTAASTPDADVCKYLETPGDSNEHAHFQKAKERLEAKHR 240
QY 329 ERMSQVMEWEAEARQAKNLPKADKAVIQHFQEKVESLEQEAANEKQQLVETINARVEA 388
DB 241 ERMSQVMEWEAEARQAKNLPKADKAVIQHFQEKVESLEQEAANEKQQLVETINARVEA 300
QY 389 MLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRHTLKHFEHVRVMDPKA 448
DB 301 MLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRHTLKHFEHVRVMDPKA 360
QY 449 AQRISQVTHLRVIERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISE 508
DB 301 AQRISQVTHLRVIERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISE 420
QY 509 PRISVGNALMPSLTETKTVELLPVNGEFSLDLQPHSFGADSVPAANTEVEPVDPAR 568
DB 421 PRISVGNALMPSLTETKTVELLPVNGEFSLDLQPHSFGADSVPAANTEVEPVDPAR 480
QY 569 PAADRGLTRPCSGLTNKTETSEISVNLDAEFHDSGYEVHHQKLVFFAEDVGSNKGAI 628
DB 481 PAADRGLTRPCSGLTNKTETSEISVNLDAEFHDSGYEVHHQKLVFFAEDVGSNKGAI 540
QY 629 GLMVGGVVIATVITVLNKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYK 688
DB 541 GLMVGGVVIATVITVLNKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYK 600
QY 689 FFEOMQN 695
DB 601 FFEOMQN 607

RESULT 12
O93296 PRELIMINARY: PRT: 534 AA.
AC O93296;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiacinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y.; Li L.; Yoshikawa K.; Schwartz L.M.; Oppenheim R.W.;
RA Milligan C.R.;
RI "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1; -.
DR #SSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 71.4%; Score 2605; DB 13; Length 534;
Best Local Similarity 94.4%; Pred. No. 8.3e-149;
Matches 504; Conservative 14; Mismatches 12; Indels 4; Gaps 3;

QY 164 NLHDYGMLLPGCIDKFRGVFVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSED 223
DB 3 NLHDYGMLLPGCIDKFRGVFVCCPLAESDNLDSDAEEDSDVMWGGADADYADGSD 62
QY 224 KVEE--VAPEEVAEEVAEEADDEDEDEVEEEAEFEPEATEERTTSIATITTTTTE 281
DB 63 KVEEESPEEDEFVTVVEDDADD--DODGDEL--EETEEPEATEERTTSIATITTTTTE 120
QY 282 SVEEVVRVPTTAASTPDADVCKYLETPGDSNEHAHFQKAKERLEAKHRMSQVMEWEAE 341
DB 121 SVEEVVRVPTTAASTPDADVCKYLETPGDSNEHAHFQKAKERLEAKHRMSQVMEWEAE 180
QY 342 ERKAKNLPKADKAVIQHFQEKVESLEQEAANEKQQLVTHHARVEAMLNDRRLALENY 401
DB 181 ERKAKNLPKADKAVIQHFQEKVESLEQEAANEKQQLVTHHARVEAMLNDRRLALENY 240
QY 402 ITALQAVPPRPHVFNMLKKYVRAEQKDRHTLKHFEHVRVMDPKAAGLRISQVTHLRV 461
DB 241 ITALQVPPRPHVFNMLKKYVRAEQKDRHTLKHFEHVRVMDPKAAGLRISQVTHLRV 300
QY 462 IYERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISEPRISVGNALMPS 521
DB 301 IYERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISEPRISVGNALMPS 360
QY 522 LTETKTVELLPVNGEFSLDLQPHSFGADSVPAANTEVEPVDPARPAADRGLTRPCS 581
DB 361 LTETKTVELLPVNGEFSLDLQPHSFGADSVPAANTEVEPVDPARPAADRGLTRPCS 420
QY 582 GLTNKTETSEISVNLDAEFHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 641
DB 421 GLTNKTETSEISVNLDAEFHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVI 480
QY 642 VITLVLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMON 695
DB 481 VITLVLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMON 534

RESULT 13
O73683 PRELIMINARY: PRT: 780 AA.
AC O73683;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE beta-amyloid protein (Beta-APP) (A-beta)].
GN App.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

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OC Tetradontolidae; Tetradontidae; Tetradont.
 OX NCBI_TaxID=47145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98252138; PubMed=959580;
 RA Villard L., Tassone F., Cirogorac-Jurcevic I., Clancy K., Gardiner K.
 RT "Analysis of zebrafish homologues of the A1-rich human APP gene."
 RL Gene 210:17-24 (1998).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GIP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
 CC BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR EMBL: AF018165; AAC41275.1; .
 DR HSP: P05067; I123.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRODOM: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; FALSE_NEG.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Serine protease inhibitor.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 780 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT CHAIN 652 724
 FT DOMAIN 19 711 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT TRANSMEM 712 732 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 733 780 POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT BPTI/KUNITZ INHIBITOR.
 FT SITE 769 772
 FT DISULFID 327 378 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 336 361 BY SIMILARITY.
 FT CARBOHYD 560 560 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;
 Query Match 70.3%; Score 2568; DB 13; Length 780;
 Best Local Similarity 65.3%; Pred. No. 2.3e+146;
 Matches 512; Conservative 71; Mismatches 95; Indels 106; Gaps 10;
 QY 7 LLLAAWTAARALEVPTDGNAGLLAEPQIAKFCGRINMHNKVNQKWSGSGTXC:DTK 66
 DB 8 LLLVAAASTLAAREVPTDVSMLLAEPQIAKFCGRINMHNKVNQKWSGSGTXC:GDK 67
 QY 67 EGILQYCEVPELQITNVVEANQPVTVQNNCKGRKCKTSPHFVTPYRCLVGEFVSDA 126
 DB 68 EGILQYCEVPELQITNVVEANQPVTVQNNCKGRKCKTSPHFVTPYRCLVGEFVSDA 127
 QY 127 LLVPDKKFLHQRNMDVCEHLHWHVAKETCEKSTNELHDYGMLLPGGIDKFRGVEVC 186
 DB 128 LLVPDKKFLHQRNMDVCEHLHWHVAKETCEKSTNELHDYGMLLPGGIDKFRGVEVC 187
 QY 137 CPLAESDNVDSADAEEDSDVWGGAGTIDVADGS-----EDKVVVEVAHFE 232
 DB 188 CP-ABEARDMDSTIEKDADDSDVWGGAGNDYSDNSKVPPEPAEQEQTREPSVVEEBEG 246

QY 233 EVAFVEEE-----ADGDEDDGDEVEERAEPEEYBEATERISIA 273
 DB 247 EVAEDDDEFEHVVLDQDQDGGHEDHAEADDEFEEDVCHTIDAPGESDDVDADPTTNWA 306
 QY 274 ---TTTITTTESVEFYVR-----
 DB 307 MTITTTITTTESVEEVMFCWAHADTGPCTASMSYFQAVDQRTMYELMYGCGGGMN 366
 QY 269 -----VPTIAASTPDVADVKYLETHGDNENHAHFOKAKERLPAKRRMSQ 333
 DB 367 NFESEYCLSVCSVVTDPSPSPDAVDHYLETAPADENHAHFOKAKESLEAKHRRMSQ 426
 QY 334 VMREWEAEAOAKNLPKADKKAVIQHFOEKVESLEGEAANEEROOLVETHMARVEAMLNDR 393
 DB 427 VMREWEAEAOAKNLPKADKKAVIQHFOEKVESLEGEAANEEROOLVETHMARVEAILNDR 486
 QY 394 RLALENYITALQAVPPRPRHVFNMLKKYVRAEOKDQHTLKHFEHVMYVDPKKAQIRS 453
 DB 487 RLALENYITALQODPPRPRHVFSLKKYVRAEQKDRQHTLKHFEHVMYVDPKKAQIRP 546
 QY 454 QVTHLRVITYERMNQSILLYNPVAVABETODEVDELLQKQNYSDVLANMISEPRISY 513
 DB 547 QVTLHRLVIERMNQSLGLLYKVGVDADTQQQV-ELLQREQAEMAQQLANLOTDVRSY 605
 QY 514 GNDALMPSLTETKTTVELLPVNGEFSUDDLOPHW--SFGADSVDPANTENEVEPVDARPA 571
 DB 606 GNDALMPDQELGQADLLP--QEDTLGGVGVHPESFN-----QLNTENQVEPVDSPFT 659
 QY 572 DRGLTTRPGSLTNIKTETISEVNLDAERHDSGYEVHHQKLVFAEDVGSNKGAIIGLM 631
 DB 660 ERGVPTRP---VTGKSMEAVPELRMETEDRQSTEVYEVHHQKLVFAEDVGSNKGAIIGLM 716
 QY 632 VGVVIATVIVITLVMLKKKQYTSIHGVVVEYDAVTPPEERHLSKMQNGYENPIYKFFE 692
 DB 717 VGVVIATVIVITLVMLKKKQYTSIHGHIEVDAVTPPEERHLSKMQNGYENPIYKFFE 776
 QY 692 QMQN 695
 DB 777 QMQN 780
 RESULT 14
 Q90W28 PRELIMINARY; PRT: 738 AA.
 AC Q90W28
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Amyloid precursor protein.
 GN APPA OR APP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 SE SEQUENCE FROM N.A.
 RA Groth C., Lardelli M.;
 RT "Expression analysis of zebrafish app.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF389401; AAK64495.1; .
 DR ZFIN: ZDB-GENE-000616-13; appa.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.

QY 653 YTSIHGVEVDAAVTPERHLSKMQNGYENPTYKFEQMON 695
DB 652 YTSIHGVEVDAAVTPERHLSKMQNGYENPTYKFEQMON 694

Search completed: October 2, 2033, 14:02:18
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:09 ; Search time 38.3333 seconds
(without alignments)
2866.063 Million cell updates/sec

Title: US-09-806-194-20

Perfect score: 3653

Sequence: 1 MLPGLALLLAWTAALV.....QQGVNPTVTFEDQMKNK 697

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3653	100.0	697	21	AA198430 Human APP695-VF-KK
2	3653	100.0	697	22	AAE10637 Human amyloid prot
3	3653	100.0	697	22	AAE06867 Human amyloid prec
4	3653	100.0	697	22	AAU06611 Human amyloid prec
5	3653	100.0	697	22	AAU07210 Human beta-amyloid
6	3653	100.0	697	22	AAE02589 Human amyloid prec
7	3653	100.0	697	23	AAE06842 Human APP695-VF-KK
8	3646	99.8	697	21	AA198428 Human APP696-KK am
9	3646	99.8	697	22	AAE10635 Human amyloid prot

10	3646	99.8	697	22	AAE05865 Human amyloid prec
11	3646	99.8	697	22	AAU06609 Human amyloid prec
12	3646	99.8	697	22	AAU07208 Human beta-amyloid
13	3646	99.8	697	22	AAE02587 Human amyloid prec
14	3646	99.8	697	23	ABB78596 APP695 mutant A-be
15	3643	99.7	695	18	AAW19498 APP695 mutant A-be
16	3643	99.7	695	18	AAW19484 APP695 mutant A-be
17	3643	99.7	695	21	AA188436 Human APP695-VF am
18	3643	99.7	695	22	AAE10634 Human amyloid prot
19	3643	99.7	695	22	AAE08864 Human amyloid prec
20	3643	99.7	695	22	AAU05608 Human amyloid prec
21	3643	99.7	695	22	AAU07207 Human beta-amyloid
22	3643	99.7	695	22	AAE02586 Human amyloid prec
23	3643	99.7	695	23	ABB78595 Human APP695-VF pr
24	3638	99.6	697	21	AA188429 Human APP695-VF am
25	3638	99.6	697	22	AAE10636 Human amyloid prot
26	3638	99.6	697	22	AAE08866 Human amyloid prec
27	3638	99.6	697	22	AAU06610 Human amyloid prec
28	3638	99.6	697	22	AAU07209 Human beta-amyloid
29	3638	99.6	697	22	AAE02588 Human amyloid prec
30	3638	99.6	697	23	ABB78597 Human APP695-Sw-KK
31	3636	99.5	695	9	APP81892 Sequence of human
32	3636	99.5	695	13	APP695. Homo sapi
33	3636	99.5	695	18	APP695 mutant A-be
34	3636	99.5	695	19	AAW19481 Human beta-amyloid
35	3636	99.5	695	20	AA197221 Amyloid precursor
36	3636	99.5	695	21	AA188434 Human APP695 amino
37	3636	99.5	695	21	AA144705 Human beta amyloid
38	3636	99.5	695	22	AAE10632 Human wild-type am
39	3636	99.5	695	22	AAE06862 Human wild-type am
40	3636	99.5	695	22	AAU06606 Human Amyloid prec
41	3636	99.5	695	22	AAE02584 Human amyloid prec
42	3636	99.5	695	23	ABG32721 Human amyloid prec
43	3636	99.5	695	23	ABB78593 Human APP695 prote
44	3636	99.5	695	23	AAE068315 Human amyloid prec
45	3636	99.5	695	24	ABB99604 Amino acid sequenc

ALIGNMENTS

RESULT 1
AA198430
ID AA198430 standard; Protein; 697 AA.

XX AA198430;

AC AA198430;

XX 03-AUG-2000 (first entry)

DT Human APP695-VF-KK amino acid sequence.

DE Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

DE Alzheimer's disease; beta secretase site; APP695-VF-KK.

XX Homo sapiens.

XX W0200017369-A2.

XX 30-MAR-2000.

XX 23-SEP-1999; 99W0-US20881.

XX 24-SEP-1998; 98US-0101594.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;

XX WPI: 2000-303209/26.

XX N-PSDB: AAA15667.

XX New enzyme designated human aspartase useful in research into

PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -
 XX Claim 133; Page 148-153; 187pp; English.
 XX This sequence represents a modified version of the human amyloid
 CC precursor protein (APP) amino acid sequence. The sequence is used in an
 CC example of the method of the invention, to show that modification of APP
 CC increases beta amyloid protein processing. The invention relates to a
 CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
 CC amyloid precursor protein (APP). The protease contains a sequence
 CC encoding the amino acid sequence DTG and a sequence encoding EDC or DTG
 CC separated by 100-1000 amino acids. When mutated the APP gene causes an
 CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
 CC surface membrane and have a single C-terminal transmembrane domain.
 CC Proteolytic processing of APP produces the amyloid beta protein, which is
 CC possibly very important in Alzheimer's disease. The invention includes a
 CC nucleotide sequence encoding the protease, a vector containing the
 CC nucleotide sequence, and a cell line comprising the vector. Methods for
 CC screening for inhibitors of beta secretase activity are also given in the
 CC invention. The human aspartase protein and nucleotide sequences and the
 CC methods for identifying inhibitors of the protease, are useful in the
 CC treatment of and research in to Alzheimer's disease.
 XX
 SQ Sequence 697 AA:
 Query Match 100.0%; Score 3653; DB 21; Length 697;
 Best Local Similarity 100.0%; Pred. No. 8,30-257;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLPGALLLAANTARALEVPTDGNAGLLAEPO:AMFGRLNMHMVQNGKWDSPGSK 60
 DB 1 MLPGALLLAANTARALEVPTDGNAGLLAEPO:AMFGRLNMHMVQNGKWDSPGSK 60
 QY 61 TCIDTKGILQYQEVYPELOITNVYFANQVPTIQNCKRGKQCKTHFHFVTPYKING 120
 DB 61 TCIDTKGILQYQEVYPELOITNVYFANQVPTIQNCKRGKQCKTHFHFVTPYKING 120
 QY 121 EFVSDALLVPDKCKFLHQESMOVCETELHHTYAKETCSKSTNLHDYCMLEPGIDKPF 180
 DB 121 EFVSDALLVPDKCKFLHQESMOVCETELHHTYAKETCSKSTNLHDYCMLEPGIDKPF 180
 QY 181 GVEFVCCPLAEDSDNVDASAEDEDDVNGGAGTLYAGSEDKVVEAESEEAVALFEEL 240
 DB 181 GVEFVCCPLAEDSDNVDASAEDEDDVNGGAGTLYAGSEDKVVEAESEEAVALFEEL 240
 QY 241 EADEDEDEDEGDEVEEAEEPEYEATEKRTSIAATTTTTSVEEYVVPPTAASTPAAV 300
 DB 241 EADEDEDEDEGDEVEEAEEPEYEATEKRTSIAATTTTTSVEEYVVPPTAASTPAAV 300
 QY 301 DKYLETPGDEHNAHFQAKERLEAKHRERMSQVNRFEAEERCAKNLPKAKKAVIQHF 360
 DB 301 DKYLETPGDEHNAHFQAKERLEAKHRERMSQVNRFEAEERCAKNLPKAKKAVIQHF 360
 QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLAENYITALQAVPPRPRIHVENMLK 420
 DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLAENYITALQAVPPRPRIHVENMLK 420
 QY 421 KYVRAEQDKQKHTLUKHFHVHVMYDPKAAQIRSQVMTLHVYTERNQSLSLYNNPVA 480
 DB 421 KYVRAEQDKQKHTLUKHFHVHVMYDPKAAQIRSQVMTLHVYTERNQSLSLYNNPVA 480
 QY 481 EEIQEVEDELLOKQFQYSDVLANMISEPRISYGNDAIMPSLTETTTVELLPVNGEFS 540
 DB 481 EEIQEVEDELLOKQFQYSDVLANMISEPRISYGNDAIMPSLTETTTVELLPVNGEFS 540
 QY 541 DDLQPHWSFGADSPANTENEVEVDARPAADRGLTTRPGSGLTNKTETSEVKKDCAF 600
 DB 541 DDLQPHWSFGADSPANTENEVEVDARPAADRGLTTRPGSGLTNKTETSEVKKDCAF 600
 QY 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLWGWGVIATVIFITLVMKKKQVTSIHGGV 660
 DB 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLWGWGVIATVIFITLVMKKKQVTSIHGGV 660

QY 661 VEYDAAVTPPERHLSKMQQNGYENPTYKFEFQMNKK 697
 DB 661 VEYDAAVTPPERHLSKMQQNGYENPTYKFEFQMNKK 697
 RESULT 2
 AAE10637
 ID AAE10637 standard; Protein: 697 AA.
 XX AAE10637:
 AC AAE10637:
 DT 10-DEC-2001 (first entry)
 XX Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.
 DE Human; aspartyl protease 1; Aspl; amyloid precursor protein;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW Amyloid plaque; neuronal loss; proteolytic; neuroprotective;
 KW APP695-VF-KK; mutant; mutain.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 642 /note= "Wild-type Val substituted with Phe"
 FT
 PN GB2357767-A.
 XX 04-JUL-2001.
 XX 22-SEP-2000; 2000GB-0023315.
 XX 23-SEP-1999; 99US-0155433.
 XX 23-SEP-1999; 99US-0404133.
 XX 23-SEP-1999; 99WO-US20881.
 XX 13-OCT-1999; 99US-0416901.
 XX 06-DEC-1999; 99US-0169232.
 XX (HNA) PHARMACIA & UPJOHN CO.
 XX Bionkowksi MZ, Gurney M:
 XX WPI: 2001-444208/48.
 XX N-PSDB: AAD17671.
 XX Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 XX Example 8: Page 120-122; 187pp; English.
 XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
 CC Aspl proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Aspl alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Aspl alpha-secretase activity, where modulators that increase
 CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
 CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Aspl proteolytic activity. The present sequence is human amyloid
 CC protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence
 CC is obtained by the addition of two lysine residues (KK motif) at
 CC the C-terminus of APP695-VF isoform which is generated by the London
 CC mutation in APP695, where Val at position 642 is replaced with Phe.
 CC APP695-VF-KK isoform is useful for assaying the beta-secretase
 CC activity of human aspartyl protease 2a (hu-Asp2a) protein.

XX	Sequence	697 AA:
SQ	Query Match	100.0%; Score 3653; DB 22; Length 697;
	Best Local Similarity	100.0%; Pred. No. 8.3e-257;
	Matches 697; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MLPGLALLLAATAWTALEVPIDGNAGLLAEPOIAMFCGRLNHNNVQKWDSPSGTK 60
DB	1	MLPGLALLLAATAWTALEVPIDGNAGLLAEPOIAMFCGRLNHNNVQKWDSPSGTK 60
QY	61	TCIDTKEGILQYCOEYVPELQITNVVEANQPTIQNWCKRGRKCKTHPHFVYPRCLVG 120
DB	61	TCIDTKEGILQYCOEYVPELQITNVVEANQPTIQNWCKRGRKCKTHPHFVYPRCLVG 120
QY	121	EFVSDALLVPDKCKFHQRMDVCFTHLHWHHTVAKETSEKSTNLHDYGMILLPCGIDKFR 180
DB	121	EFVSDALLVPDKCKFHQRMDVCFTHLHWHHTVAKETSEKSTNLHDYGMILLPCGIDKFR 180
QY	181	GVEFVCCPLAEESDNDSDACAEEDSDVWVGADTDYADGSDKVVVEAESEVAEVEE 240
DB	181	GVEFVCCPLAEESDNDSDADAEEDSDVWVGADTDYADGSDKVVVEAESEVAEVEE 240
QY	241	EADDDDEDDGDEVEAEAEPEEATERITTSIATITTTTESVEEVVPTTAASTPDVAV 300
DB	241	EADDDDEDDGDEVEAEAEPEEATERITTSIATITTTTESVEEVVPTTAASTPDVAV 300
QY	301	DKYLETPGDENEHAHFQAKERLEAKHRERMSOVWREWEAEERQAKNLKADKAVIQHF 360
DB	301	DKYLETPGDENEHAHFQAKERLEAKHRERMSOVWREWEAEERQAKNLKADKAVIQHF 360
QY	361	QEKVESLEQEAANERQOLVETHHARVEAMLNDRKLALENYITALOAVPRPRHFVNMJK 420
DB	361	QEKVESLEQEAANERQOLVETHHARVEAMLNDRRLALENYITALOAVPRPRHFVNMJK 420
QY	421	KYVRAEQKQROHTLKHFRVHMVDPKKAQIRSOVMTHLRVIYERNQSLSLLYNPAVA 480
DB	421	KYVRAEQKQROHTLKHFRVHMVDPKKAQIRSOVMTHLRVIYERNQSLSLLYNPAVA 480
QY	481	BEIQDEVELLQEQNYSDVLANMISEPRISYGNDAKPSLTETTTVELLPVNGEFSI 540
DB	481	BEIQDEVELLQEQNYSDVLANMISEPRISYGNDAKPSLTETTTVELLPVNGEFSI 540
QY	541	DLQPHSHSGADSVPAANTENEVEPVDARPAADRLTRPGSGLTNKTETFEISEVKMDAEF 600
DB	541	DLQPHSHSGADSVPAANTENEVEPVDARPAADRLTRPGSGLTNKTETFEISEVKMDAEF 600
QY	601	RHDSGYEVHQQKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITLYMLKKKQYTSIHGCV 660
DB	601	RHDSGYEVHQQKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITLYMLKKKQYTSIHGCV 660
QY	661	VEYDAAVTPFERHLSKMQQNGYENPTYKTFEOMONKK 697
DB	661	VEYDAAVTPFERHLSKMQQNGYENPTYKTFEOMONKK 697
RESULT 3		
AAE06867		
ID	AAE06867	standard: Protein; 697 AA.
XX	AAE06867;	
AC		
XX		
DT	23-OCT-2001	(first entry)
XX		
DE	Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.	
XX		
KW	Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF-KK;	
KW	beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;	
KW	neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;	
KW	neuroprotective; antisense therapy; gene therapy; APP695-VF-KK; mutant;	
XX		
OS	Homo sapiens.	

361 QEKVESLEQEAANERQQLVETHMARVCAMLNDRRLALENYITLQAVPPRPFRHVFNNLK 420
 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSQVMTSLRVIVYERMNQSLSLVYVPAVA 480
 422 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSQVMTSLRVIVYERMNQSLSLVYVPAVA 480
 481 EEIQDEVDLQKQNTSDVCAAMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
 481 EEIQDEVDLQKQNTSDVCAAMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
 541 DDLOPWHSGADSVPAANTENEPVDARPAADRGITTPGSGSLTNIKTEISEVKMDAEF 600
 541 DDLOPWHSGADSVPAANTENEPVDARPAADRGITTPGSGSLTNIKTEISEVKMDAEF 600
 601 RHDSGYEVHHOKLVFFAEDVGSNGKGAIGLVGGVVIATVIFITLMLKKQYTSIHGV 660
 601 RHDSGYEVHHOKLVFFAEDVGSNGKGAIGLVGGVVIATVIFITLMLKKQYTSIHGV 660
 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMKNK 697
 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMKNK 697

RESULT 5
 AAU07210 standard: Protein.: 697 AA.

AAU07210;
 24-OCT-2001 (first entry)
 Human beta-amyloid protein precursor, APP695-VF-KK.
 Human: aspartyl protease 1; Asp-1; nootropic; neuroprotective;
 aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 beta-secretase; Alzheimer's disease; APP695-VF-KK.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 642 /note= "Wild type Val substituted by Phe"
 FT
 PN WO200149097-A2.
 PD 12-JUL-2001.
 XX 09-MAY-2001: 2001WO-1B00797.
 PR 09-MAY-2001: 2001WO-1B00797.
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 WPI: 2001-502548/55.
 DR N-PSDB; AAS11710.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 PS Example 8: Page 150-152; 185pp; English.
 XX The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2

protein. Also included is an isoform of amyloid protein precursor (APP) comprising the amino acid sequence of a APP or its fragment containing an APP cleavage site recognisable by a mammalian beta-secretase, and further comprising two lysine residues at the carboxyl terminus of the amino acid sequence of the mammalian APP or APP fragment. The polypeptides are used for assaying for modulators of beta-secretase activity; identifying agents that inhibit the APP processing activity of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that modulate the activity of Asp2; and for reducing cellular production of amyloid beta (Abeta) from APP. Agents identified by the above methods are useful for treating Alzheimer's disease; and for identifying modulators of amyloid-beta (Abeta) peptide production, for use in designing therapeutics for the treatment or prevention of Alzheimer's disease. Probes and primers derived from Asp nucleic acid sequences are useful for detecting Hu-Asp nucleic acids in vitro assays and in Northern and Southern blots. The present sequence represents the amino acid sequence of human amyloid protein precursor, APP695-VF-KK, used in the method of the invention.

XX Sequence 697 AA:

Query Match 100.0%; Score 3653; DB 22; Length 697;
 Best Local Similarity 100.0%; Pred. No. 8.3e-257;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLPGALLLLAAMTARALFVPTDGNAGLLAEPOIAMFCGRNLNHNHNQVCKWDSFGTK 60
 DB 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNHNQVCKWDSFGTK 60
 QY 61 TCIDTRGILQYCOEYVPELQITNVYEAOPVTIONNCKRQCKTHPHFVPIYRCLVG 120
 DB 61 TCIDTRGILQYCOEYVPELQITNVYEAOPVTIONNCKRQCKTHPHFVPIYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCEHHLHWHTVAKETCSEKSTNLHDYGLLPCGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCEHHLHWHTVAKETCSEKSTNLHDYGLLPCGIDKFR 180
 QY 181 GVFEVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 DB 181 GVFEVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 QY 241 EADDEDDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVVRVPTTAASPTDAV 300
 DB 241 EADDEDDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVVRVPTTAASPTDAV 300
 QY 301 DKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEAKNLPKADKKAVIQHF 360
 DB 301 DKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEAKNLPKADKKAVIQHF 360
 QY 361 QEKVESLEQEAANERQQLVETHMARVCAMLNDRRLALENYITLQAVPPRPFRHVFNNLK 420
 DB 361 QEKVESLEQEAANERQQLVETHMARVCAMLNDRRLALENYITLQAVPPRPFRHVFNNLK 420
 QY 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSQVMTSLRVIVYERMNQSLSLVYVPAVA 480
 DB 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSQVMTSLRVIVYERMNQSLSLVYVPAVA 480
 QY 481 EEIQDEVDLQKQNTSDVCAAMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
 DB 481 EEIQDEVDLQKQNTSDVCAAMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
 QY 541 DDLOPWHSGADSVPAANTENEPVDARPAADRGITTPGSGSLTNIKTEISEVKMDAEF 600
 DB 541 DDLOPWHSGADSVPAANTENEPVDARPAADRGITTPGSGSLTNIKTEISEVKMDAEF 600
 QY 601 RHDSGYEVHHOKLVFFAEDVGSNGKGAIGLVGGVVIATVIFITLMLKKQYTSIHGV 660
 DB 601 RHDSGYEVHHOKLVFFAEDVGSNGKGAIGLVGGVVIATVIFITLMLKKQYTSIHGV 660
 QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMKNK 697
 DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMKNK 697

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RESULT 6
AAE02589
ID AAE02589 standard; Protein: 697 AA.
XX
AC AAE02589;
D- 10-AUG-2001 (first entry)
XX
XX Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).
XX
XX Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;
KW APP695-VF-KK; Alzheimer's disease; Alzheimer's.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN W0200123533-A2.
XX
PD 05-APR-2001.
XX
XX 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Gurney M, Bienkowski MJ;
XX
XX WPI: 2001-290516/30.
XX
XX N-PSDB; AAD06747.
XX
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX protein, useful for the treatment of Alzheimer's disease.
XX
XX Example 8; Page 143-151; 189pp; English.
XX
XX The present invention relates to enzymes for cleaving the alpha-
XX secretase site of the amyloid precursor protein (APP) and methods of
XX identifying those enzymes. The methods may be used to identify enzymes
XX that may be used to cleave the alpha-secretase cleavage site of the APP
XX protein. The enzymes may be used to treat or modulate the progress of
XX Alzheimer's disease. The present sequence is human APP695-VF-KK. This
XX sequence is characterised by a V to F alteration at position 642
XX and contains two carboxy-terminal lysine residues.
XX
XX Sequence 697 AA:
XX
XX Query Match 100.0%; Score 3653; DB 22; Length 697;
XX Best Local Similarity 100.0%; Pred. No. 8,30-257;
XX Matches 697; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLEGLALLLLAANTARALEVPTDGNAGLLAEPDIAFMFCGRJNNHMMVQNGKWDSPGSK 60
XX DB 1 MLEGLALLLLAANTARALEVPTDGNAGLLAEPDIAFMFCGRJNNHMMVQNGKWDSPGSK 60
XX
XX QY 61 TCIDTREGILYCOEVYPEQITNVVEANOPVTIQNWKCKGRKCKTHPHFVTPYSCVAG 120
XX DB 61 TCIDTREGILYCOEVYPEQITNVVEANOPVTIQNWKCKGRKCKTHPHFVTPYSCVAG 120
XX
XX QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTYAKETCSKSTNLDYGMILPCGIDKFR 180
XX DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTYAKETCSKSTNLDYGMILPCGIDKFR 180
XX
XX QY 181 GVEFVCCPLAESNDVSDAEDDDSDVMWGGADTDYADGSDKVEVEAEVEAEVEE 240
XX DB 181 GVEFVCCPLAESNDVSDAEDDDSDVMWGGADTDYADGSDKVEVEAEVEAEVEE 240
XX
XX QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTITTESVEEVVVPVTTAASPDVA 300
XX

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DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTITTESVEEVVVPVTTAASPDVA 300
QY 301 DKYLEIPGDENEHAHFQAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVIQHF 360
DB 361 DKYLEIPGDENEHAHFQAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 OEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITALQAVPPRPHVFNMLK 420
DB 421 KYVRAEQKDRQHTLKHFEHVRWVDPKAAQIRSQVMTHLRVYIERMNGSLLYNVPVAV 480
DB 481 KYVRAEQKDRQHTLKHFEHVRWVDPKAAQIRSQVMTHLRVYIERMNGSLLYNVPVAV 480
QY 481 BEIODEVDELLOKEONYSDDLANNMISPEPISYNDALMPSLTETKTIVELLVNGEFS 540
DB 541 BEIODEVDELLOKEONYSDDLANNMISPEPISYNDALMPSLTETKTIVELLVNGEFS 540
QY 541 DDLQPHSHFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEYKMDAEF 600
DB 601 DDLQPHSHFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEYKMDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITLMLKKQYTSIHGV 660
DB 601 RHDGSEYVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITLMLKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697

RESULT 7
ABB78598
ID ABB78598 standard; Protein: 697 AA.
XX
AC ABB78598;
XX
XX 16-JUL-2002 (first entry)
XX
XX Human APP695-VF-KK protein sequence SEQ ID NO:20.
XX
XX Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
XX proteolytic; amyloid precursor protein; APP.
XX
XX Homo sapiens.
XX
XX G52367050-A.
XX
XX 27-MAR-2002.
XX
XX 29-OCT-2001; 2001GB-C025934.
XX
XX 23-SEP-1999; 99US-155493P.
XX
XX 23-SEP-1999; 99US-0404133.
XX
XX 23-SEP-1999; 99WO-US20881.
XX
XX 13-OCT-1999; 99US-0416901.
XX
XX 06-DEC-1999; 99US-169232P.
XX
XX 22-SEP-2000; 2000GB-C023315.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Bienkowski MJ, Gurney M;
XX
XX WPI: 2002-396337/43.
XX
XX N-PSDB; ABL52465.
XX
XX Human aspartyl protease 1 substrates useful in assays to detect
XX aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
XX disease.
XX
XX Example 8; Page 120-122; 182pp; English.
XX
XX The present invention describes a human aspartyl protease 1 (hu-Asp1)

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CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC G-u-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (1) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the
CC non-coding strand complementary to a defined 1804 nucleotide sequence
CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain; (3) a purified polynucleotide (IV) comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB76839)); (4) a vector (IV)
CC comprising (III) or (III') and (5) a host cell (V) transformed or
CC transcribed with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents human amyloid precursor protein APP695-VF-KK, which
CC is given in an example from the present invention.

XX Sequence 697 AA;

Query Match 100.0%; Score 3653; DB 23; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.3e-257;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYQNGKWDSPSGTK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYQNGKWDSPSGTK 60
QY 61 TCIDTKGILQYCEVYPELQITNVVEANQPVTIQNMCKRGKCKOCTHPHFVTPYRCLVG 120
DB 61 TCIDTKGILQYCEVYPELQITNVVEANQPVTIQNMCKRGKCKOCTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 161 GVEFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 161 GVEFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDEDEDEGDEVEEAEEPEEATERTTSIATITTTTTSVEEVVRVPTTAASTPDV 300
DB 241 EADDEDEDEGDEVEEAEEPEEATERTTSIATITTTTTSVEEVVRVPTTAASTPDV 300
QY 301 DKYLETGDENEHAHFQAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVTQHF 360
DB 301 DKYLETGDENEHAHFQAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVTQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRVFNKLEK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRVFNKLEK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTFLRVYERMNQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTFLRVYERMNQSLSLYNVPAVA 480
QY 481 EEIQDEVELLQKQNYSDVLANMISEPRIISYNDALMPSLTETKTVELLPVNGEFSL 540
DB 481 EEIQDEVELLQKQNYSDVLANMISEPRIISYNDALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLQPMHSFGADSPANTENEVEVPDAPADRGLTTPGSGSLNINTEFEISEVKMDAEF 600
DB 541 DDLQPMHSFGADSPANTENEVEVPDAPADRGLTTPGSGSLNINTEFEISEVKMDAEF 600
QY 601 RDSGYEVHHQKLVFFAEDEVGSNKGAIIGLMVGWGIATVFTITLVMKKKQYTSIHGV 660
DB 601 RDSGYEVHHQKLVFFAEDEVGSNKGAIIGLMVGWGIATVFTITLVMKKKQYTSIHGV 660

QY 661 VEYDAAVIPEERHLSKMQNGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVIPEERHLSKMQNGYENPTYKFFEQMNKK 697

RESULT 2

AA598428
ID AAY98428 standard; Protein: 697 AA.

AC AAY98428;

DT 03-AUG-2000 (first entry)

LE Human APP696-KK amino acid sequence.

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP696-KK.

OS Homo sapiens.

PN W0200017369-A2.

PD 30-MAR-2000.

PF 23-SEP-1999; 59WK0-US20881.

PP 24-SEP-1998; 98US-0101594.

PA (PHAA) PHARMACIA & UPJOHN CO.

PI Gurney ME, Bienkowski MJ, Heinrichson RJ, Parodi LA, Yan R;

DR WPI: 2000-303209/26.

XX N-PSDB; AAA15665.

PI New enzyme designated human aspartase useful in research into
PI Alzheimer's disease is capable of cleaving amyloid protein precursor at
PI the beta secretase site to produce amyloid beta peptide -

PS Claim 132; Page 137-141; 183pp; English.

CC This sequence represents a modified version of the human amyloid
CC precursor protein (APP) amino acid sequence. The sequence is used in an
CC example of the method of the invention, to show that modification of APP
CC increases beta amyloid protein processing. The invention relates to a
CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
CC amyloid precursor protein (APP). The protease contains a sequence
CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
CC separated by 100-300 amino acids. When mutated the APP gene causes an
CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
CC surface membrane and have a single C-terminal transmembrane domain.
CC Proteolytic processing of APP produces the amyloid beta protein, which is
CC possibly very important in Alzheimer's disease. The invention includes a
CC nucleotide sequence encoding the protease, a vector containing the
CC screening for inhibitors of beta secretase activity are also given in the
CC invention. The human aspartase protein and nucleotide sequences and the
CC methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease.

XX Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 21; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.7e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYQNGKWDSPSGTK 60

DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYQNGKWDSPSGTK 60

QY 61 TCIDTKGILQYCEVYPELQITNVVEANQPVTIQNMCKRGKCKOCTHPHFVTPYRCLVG 120
|||||

Db 61 TCIDTKEGILQYCEVYPPELQITNVVEANQPV:IQNWCKRGRKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSNLHXYGMLLPCGICKR 280
Db 122 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSNLHXYGMLLPCGICKR 280
QY 181 GVEFYCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
Db 181 GVEFYCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPPTAASPDV 300
Db 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPPTAASPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREWEAEERQAKNLPKADKAVIOHF 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
QY 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Db 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDQLQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGGLTNITKTEISEVKNDAEF 600
Db 541 DDQLQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGGLTNITKTEISEVKNDAEF 600
QY 601 RHDGSGYEVHHQKLVFFAEVDGSKNGATIGLWGGVIAIVIFILVLVKKKQVTSIHHGV 660
Db 601 RHDGSGYEVHHQKLVFFAEVDGSKNGAIIGLWGGVIAIVITVLVKKKQVTSIHHGV 660
QY 661 VEYDAVTPPEERHLSKMQONGYENPTYKFFEOQNK 697
Db 661 VEYDAVTPPEERHLSKMQONGYENPTYKFFEOQNK 697

RESULT 9
AAE10635

ID AAE10635 standard; Protein: 697 AA.

AC AAE10635;

XX AAE10635;

DT :0-DEC-2001 (first entry)

DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.

XX Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KX amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective.

OS Homo sapiens.

OS Synthetic.

XX GB2357767-A.

XX 04-JUL-2001.

XX 22-SEP-2000; 2000GB-0023315.

XX 23-SEP-1999; 99US-0155493.

PR 23-SEP-1999; 99US-0404133.

PR 23-SEP-1999; 99WO-0520881.

PR 13-OCT-1999; 99US-0416901.

PR 06-DEC-1999; 99US-0169232.

XX (PRAA) PHARMACIA & UPJOHN CO.

XX BIENKOWSKI MJ, Gurney M;
XX WPI; 2001-444208/46.
DR N-PSDB: AAD17871.
XX Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX Example 6: Page 114-116; 187pp; English.
XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC Aspl proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Aspl alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-KK (APP695-KK) isoform which is obtained by
CC the addition of two Lys residues (KK motif) at the C-terminus of
CC APP695 protein.
XX Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 22; Length 697;
Best local Similarity 99.9%; Pred. No. 2,7e+256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEFQIAMFCGRLLMHNQVNGKWDSPSCTK 60
DB 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEFQIAMFCGRLLMHNQVNGKWDSPSCTK 60
QY 61 TCIDTKEGILQYCEVYPPELQITNVVEANQPV:IQNWCKRGRKQCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCEVYPPELQITNVVEANQPV:IQNWCKRGRKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSNLHXYGMLLPCGICKR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSNLHXYGMLLPCGICKR 180
QY 181 GVEFYCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
DB 181 GVEFYCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPPTAASPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPPTAASPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREWEAEERQAKNLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
QY 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
DB 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540

QY 541 DDLPWHSGADSVPAANTEVEPVDARPAADAGLTTRPGSLINIKTEISFVKMADE 600
Db 541 DDLPWHSGADSVPAANTEVEPVDARPAADAGLTTRPGSLINIKTEISFVKMADE 600
QY 601 RHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVIFILVLMKKKQYTSIHVG 600
Db 601 RHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVIFILVLMKKKQYTSIHVG 600
QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMNKK 697

RESULT 10
AAU06609
ID AAU06609 standard; Protein: 697 AA.
AC AAU06609;
DT 23-OCT-2001 (first entry)
XX Human amyloid precursor protein 695-KK (APP695-KK) isoform.
XX Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neuroprotection; antisense therapy; gene therapy; APP695-KK; mutant;
KW muten.
XX Homo sapiens.
OS Homo sapiens.
XX W0200150829-A2.
PN W0200150829-A2.
XX 19-JUL-2001.
PD 19-JUL-2001.
XX 09-MAY-2001; 2001WO-IB00799.
PF 09-MAY-2001; 2001WO-IB00799.
XX 09-MAY-2001; 2001WO-IB00799.
PR 09-MAY-2001; 2001WO-IB00799.
XX (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
PI Bienkowski MJ, Gurney ME, Heinrikson R., Parodi LA, Yan R;
XX WPI; 2001-483072/52.
DR N-PSDB; AAD13027.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PI protease 2, lacking Asp2 transmembrane domain and retaining beta
PI secretase activity of Asp2 useful for identifying inhibitors of Asp2
PI activity
XX
XX Example 6; Page 144-146; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. App isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present sequence is modified human amyloid precursor

CC protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
CC addition of two lys residues (KK motif) at the C-terminal end of APP695
CC isoform.
XX
SQ Sequence 697 AA;
Query Match 99.8%; Score 3646; DB 22; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.7e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEQIAFMFCGRLNHNHNVQNGKSDSPSGTK 60
Db 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEQIAFMFCGRLNHNHNVQNGKSDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYYPQLQITNVVEANQPTVIONWCKRGRKQCKTHPHFVPIRCLVG 120
Db 61 TCIDTKEGILQYCOEYYPQLQITNVVEANQPTVIONWCKRGRKQCKTHPHFVPIRCLVG 120
QY 121 EFVSDALAVPDKCKFLQERMDVCETHLHWHIVAKETSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALAVPDKCKFLQERMDVCETHLHWHIVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSECKVVEAEVEAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSECKVVEAEVEAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEEATERTTSIATITTTTESVEEVVRVPTTAASDPDAV 300
Db 241 EADDDEDDGDEVEEAEPEEATERTTSIATITTTTESVEEVVRVPTTAASDPDAV 300
QY 301 DKYLETTPGDENEHAHFQKAKERLEAKHRERMSQVREWEAEERAKNLPKADKAVIQHF 360
Db 301 DKYLETTPGDENEHAHFQKAKERLEAKHRERMSQVREWEAEERAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETIHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQOLVETIHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSOVMTHLRVIYERNQSLSLYNNPVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSOVMTHLRVIYERNQSLSLYNNPVA 480
QY 481 EETQDEVEDELQKQNYSDVLANMISEPRISVGNDAIMPSTETKTVELLPVNGEFSL 540
Db 481 EETQDEVEDELQKQNYSDVLANMISEPRISVGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDLQPHWSEGADSVPAANTEVEPVDARPAADAGLTTRPGSLINIKTEISEVKMDAEF 600
Db 541 DDLQPHWSEGADSVPAANTEVEPVDARPAADAGLTTRPGSLINIKTEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVIFILVLMKKKQYTSIHVG 660
Db 601 RHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVIFILVLMKKKQYTSIHVG 660
QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMNKK 697

RESULT 11
AAU06609
ID AAU06609 standard; Protein: 697 AA.
AC AAU06609;
DT 24-OCT-2001 (first entry)
XX Human Amyloid precursor protein mutant, APP695-KK.
XX Human; Aspartyl protease; Asp2b; beta-secretase; neurotropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; APP695-KK; mutant; muten.
XX

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 696..697
 FT /note= "2 Extra Lys residues added compared to
 FT wild-type APP695"
 XX
 XX WC200149098-A2.
 XX
 XX 12-JUL-2001.
 XX
 XX 09-MAY-2001; 2001WO-IB00797.
 XX
 XX 09-MAY-2001; 2001WO-IB00797.
 XX
 XX (BIEN/) BIENKOWSKI M J.
 XX (GURN/) GURNEY M E.
 XX (HEIN/) HEINRIKSON R L.
 XX (PARO/) PARODI L A.
 XX (YANR/) YAN R.
 XX
 XX Blenkowski MJ, Gurney MF, Heinrichson RL, Parodi LA, Yan R;
 XX WPI: 2001-502549/55.
 XX N-PSDB; AAS11523.
 XX
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX
 XX Example 6: Page 144-146; i85pp; English.
 XX
 XX The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp2) protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the App-Sw-beta-secretase peptide sequence (N2A), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC Asp oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is the human
 CC APP695 mutant, APP695-KK which has 2 extra Lys residues added at
 CC the C-terminus compared to the wild-type APP695. The mutation alters the
 CC specificity of the APP gamma-secretase activity and increases the rate
 CC of processing of the amyloid Abeta peptide.
 XX
 XX Sequence 697 AA:
 SQ
 Query Match 99.8%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 2.7e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAATAALEVPTDGNAGLLAEPIQAFMFCGLRNHNMVQNGKWDSPSGTK 60
 DB 1 MLPGLALLLAATAALEVPTDGNAGLLAEPIQAFMFCGLRNHNMVQNGKWDSPSGTK 60
 QY 61 TCIDTKEGILQYCOEVYPELQITNVVEANOPVTIONMCKRCKOCKTHPHFVPIYRCLVG 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 61 TCIDTKEGILQYCOEVYPELQITNVVEANOPVTIONMCKRCKOCKTHPHFVPIYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLHHTVAKETCSEKSTKLHDYGMGLPGIDKFR 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLHHTVAKETCSEKSTKLHDYGMGLPGIDKFR 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 GVEFVCCPLAEESDNVSADAEEDSDVMWGGADTDYADGSEDPKVVVAAVEEFVAAVEEE 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 GVEFVCCPLAEESDNVSADAEEDSDVMWGGADTDYADGSEDPKVVVAAVEEFVAAVEEE 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 EADDEDDEGDEVEEEAEPEYEATERTTSIATITTTTIESVEEVVVRVPTTAASTPIAV 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 EADDEDDEGDEVEEEAEPEYEATERTTSIATITTTTIESVEEVVVRVPTTAASTPIAV 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 DKYLETGGDENEHAHFOKAKEKLEAKHPRMSQVMREWEAEARQAKNLPRADKKAVTOHF 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 DKYLETGGDENEHAHFOKAKEKLEAKHPRMSQVMREWEAEARQAKNLPRADKKAVTOHF 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 KYRAEQKDRQHTLKFHFHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNPVA 480
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 KYRAEQKDRQHTLKFHFHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNPVA 480
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 EEIODEVELLQKQSONYSDOVLANMISEPRISYNDALMPSLTETKTIVELLPVNGEFSL 540
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 481 EEIODEVELLQKQSONYSDOVLANMISEPRISYNDALMPSLTETKTIVELLPVNGEFSL 540
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 541 DDLOPWHSPGADSVPAANTENEVEPVDARPAADRLTTRPGSGLTNIKTEEISEVKMDAEF 600
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 541 DDLOPWHSPGADSVPAANTENEVEPVDARPAADRLTTRPGSGLTNIKTEEISEVKMDAEF 600
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 601 RHDGSEYVHHOKLVFFAEADVGSNGKAGIIGLMVGGVVIATVIFILVLMKKQYTSIHGV 660
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 601 RHDGSEYVHHOKLVFFAEADVGSNGKAGIIGLMVGGVVIATVIFILVLMKKQYTSIHGV 660
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMONKK 697
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 661 VEVDAAVTPEERHLSKMOQNGYENPTYKFFEQMONKK 697
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 12
 AAU07208
 IC AAU07208 standard; Protein: 697 AA.
 XX AAU07208;
 XX
 XX 24-OCT-2001 (first entry)
 XX Human beta-amyloid protein precursor, APP695-KK.
 DE
 XX Human; aspartyl protease 2; Asp-1; notropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KW beta-secretase; Alzheimer's disease; APP695-KK.
 XX
 CS Homo sapiens.
 XX
 XX WC200149097-A2.
 XX
 XX 12-JUL-2001.
 XX
 XX 09-MAY-2001; 2001WO-IB00797.
 XX
 XX 09-MAY-2001; 2001WO-IB00797.
 XX
 XX (BIEN/) BIENKOWSKI M J.
 XX (GURN/) GURNEY M E.
 XX (HEIN/) HEINRIKSON R L.
 XX (PARO/) PARODI L A.
 XX (YANR/) YAN R.
 XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX WPI: 2001-502548/55.
 DR N-PSDB; AAS11708.
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX
 PS Example 6; Page 144-146; 185pp; English.
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protease, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, Asp695-KK.
 XX used in the method of the invention.
 XX
 SQ Sequence 697 AA;

Query Match 99.88; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.98; Pred. No. 2.7e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAAMFCGRNLNMHMYQNGKWSDFSGTK 60
 Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAAMFCGRNLNMHMYQNGKWSDFSGTK 60

Qy 61 TCIDTKESILQYCOEYVPELQITNVVPAQVPIQWCKKGRKCKTTPHPIVPIRCLVG 120
 Db 61 TCIDTKESILQYCOEYVPELQITNVVPAQVPIQWCKKGRKCKTTPHPIVPIRCLVG 120

Qy 121 EFVSDALLVPKCKFLHQRWQVCEHLHWHIVAKETCSFKSTN:HDYGMCLPGLIDKFR 180
 Db 121 EFVSDALLVPKCKFLHQRWQVCEHLHWHIVAKETCSFKSTN:HDYGMCLPGLIDKFR 180

Qy 181 GVEFVCCPLAESNDVSADAEEDSDVWNGGADTVYADGSEDKVVFVAEEVAEVEE 240
 Db 181 GVEFVCCPLAESNDVSADAEEDSDVWNGGADTVYADGSEDKVVFVAEEVAEVEE 240

Qy 241 EAUDDEDEGDGDEVEEAEPEEATERTTSIATTTTTSVEFVVRVPTIAASTPDVAV 300
 Db 241 EAUDDEDEGDGDEVEEAEPEEATERTTSIATTTTTSVEFVVRVPTIAASTPDVAV 300

Qy 301 DKYLETGDENEHAHFCKAKERLEAKRERMSQVNRWEEAEERQAKNLPKADKAVIQHF 360
 Db 301 DKYLETGDENEHAHFCKAKERLEAKRERMSQVNRWEEAEERQAKNLPKADKAVIQHF 360

Qy 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPVFNMLK 420
 Db 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPVFNMLK 420

Qy 421 KYVRAEQKDRQHTLUKHEHVRWMDPKKAAQIRSOVNTHLRVIYERMQSISLIYNPVA 480
 Db 421 KYVRAEQKDRQHTLUKHEHVRWMDPKKAAQIRSOVNTHLRVIYERMQSISLIYNPVA 480

Qy 481 EETQDEVDELLOKEQNSDDVLANKISEPRIISYGNALMPSLTETKTTVELLPVNGEFL 540
 Db 481 EETQDEVDELLOKEQNSDDVLANKISEPRIISYGNALMPSLTETKTTVELLPVNGEFL 540

Qy 541 DDLQPHSFSGADSVPAANTENEVEPVDARPAADRGLTIRPGSLTNIKTEEISEVKMDAEF 600
 Db 541 DDLQPHSFSGADSVPAANTENEVEPVDARPAADRGLTIRPGSLTNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVSHQKLVFPFAEDVGSNGKCAIGLMVGGVVIATVITILVWLKKQYTSIHGGV 660
 Db 601 RHDSGYEVSHQKLVFPFAEDVGSNGKCAIGLMVGGVVIATVITILVWLKKQYTSIHGGV 660

Qy 661 VEVDAAVTPEERHLSKMQONGYENPIYKFFEOMONKK 697
 Db 661 VEVDAAVTPEERHLSKMQONGYENPIYKFFEOMONKK 697

RESULT 13
 AAE02587
 ID AAE02587 standard; Protein; 697 AA.
 XX
 AC AAE02587;
 DT 10-AUG-2001 (first entry)
 DE Human amyloid precursor protein 695-KK (APP695-KK).
 XX
 KW Human: alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
 KW therapy; Alzheimer's disease; antialzheimer's.
 XX Homo sapiens.
 OS Synthetic.
 XX KW020123533-A2.
 XX
 XX 05-APR-2001.
 XX 22-SEP-2000; 2000WO-US26080.
 XX
 XX 23-SEP-1999; 99US-0155493.
 XX 23-SEP-1999; 99WO-US20881.
 XX 13-OCT-1999; 99US-0416901.
 XX 06-DEC-1999; 99US-0169232.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Gurney M, Bienkowski MJ;
 XX WPI: 2001-290516/30.
 XX N-PSDB; AAD06745.
 XX
 XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
 XX protein, useful for the treatment of Alzheimer's disease -
 XX
 XX Example 6; Page 143-145; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human APP695-KK. This
 CC sequence contains two carboxy-terminal lysine residues.
 XX
 SQ Sequence 697 AA;

Query Match 99.88; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.98; Pred. No. 2.7e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAAMFCGRNLNMHMYQNGKWSDFSGTK 60
 Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAAMFCGRNLNMHMYQNGKWSDFSGTK 60

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QY 61 TCIDTKESILQYCOEYVPELOITNNVEANOPVTIONMCKRGKQCKTHPHFVPIRCLVG 120
DB 61 TCIDTKESILQYCOEYVPELOITNNVEANOPVTIONMCKRGKQCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQEMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQEMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSEKVVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSEKVVVEAEVEEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVPTTAASTPDAY 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVPTTAASTPDAY 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSOVMRWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSOVMRWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVMDPKKAAQIRSOVMTHLRVIYERNQSLSLLYNPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVMDPKKAAQIRSOVMTHLRVIYERNQSLSLLYNPAVA 480
QY 481 EEIODEVELLOKEQNSYSDVLANMISEPRISYGNALMPSJTEKTITVELLPVNGEFSL 540
DB 481 EEIODEVELLOKEQNSYSDVLANMISEPRISYGNALMPSJTEKTITVELLPVNGEFSL 540
QY 541 DDLOPHSHFGADSVPAANTEVEPVDARPAADRGLTTRPGSLTNKIKTEISEVKNDAEF 600
DB 541 DDLOPHSHFGADSVPAANTEVEPVDARPAADRGLTTRPGSLTNKIKTEISEVKNDAEF 600
QY 601 RHDSGEVHHOKLVFFAEDYGSNKGAIIGLMWGGVVIATVIFITLVMLKKKQYTSIHGGV 660
DB 601 RHDSGEVHHOKLVFFAEDYGSNKGAIIGLMWGGVVIATVIFITLVMLKKKQYTSIHGGV 660
QY 661 VEYDAAVTPERHLKSKQNGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPERHLKSKQNGYENPTYKFFEQMNKK 697
RESULT 14
ID ABB78596
XX ABB78596 standard; Protein: 597 AA.
AC ABB78596;
XX ABB78596;
DT 16-JUN-2002 (first entry)
XX
DB Human AP695-KK protein sequence SEQ ID NO:16.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic; amyloid precursor protein; APP.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
DB 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-6404133.
PR 13-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.

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XX (PHAA ) PHARMACIA & UPJOHN CO.
XX Bienkowski MJ, Gurney M;
XX WPI: 2002-396337/43.
XX N-PSDB: ABL52463.
XX Human aspartyl protease 1 substrates useful in assays to detect
XX aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
XX disease.
XX
XX Example 6: Page 114-116; 182pp; English.
XX
XX The present invention describes a human aspartyl protease 1 (hu-Aspl)
XX substrate (I) which comprises a peptide of no more than 50 amino acids,
XX and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-
XX Glu-Pro. Also described are: (1) a method (II) for assaying hu-Aspl
XX proteolytic activity, comprising: (a) contacting a hu-Aspl protein with
XX (1) under acidic conditions; and (b) determining the level of hu-Aspl
XX proteolytic activity; (2) a purified polynucleotide (III) comprising a
XX nucleotide sequence that hybridises under stringent conditions to the
XX non-coding strand complementary to a defined 1804 nucleotide sequence
XX (see ABL52456) where the nucleotide sequence encodes a polypeptide having
XX Aspl proteolytic activity and lacks nucleotides encoding a transmembrane
XX domain; (3) a purified polynucleotide (III') comprising a sequence that
XX hybridises under stringent conditions to (III) (the nucleotide sequence
XX encodes a polypeptide further lacking a pro-peptide domain corresponding
XX to amino acids 23-62 of hu-Aspl (see ABB78589)); (4) a vector (IV)
XX comprising (III) or (III'); and (5) a host cell (V) transformed or
XX transfected with (III), (III') and/or (IV). The hu-Aspl protease
XX substrate (I) may be used as an enzyme substrate in assays to detect
XX aspartyl protease activity, (II) and therefore diagnose diseases
XX associated with aberrant hu-Aspl expression and activity such as
XX Alzheimer's disease. Hu-Aspl has been localised to chromosome 21, while
XX hu-Asp2 has been localised to chromosome 11q23.3-24.1; the present
XX sequence represents human amyloid precursor protein APP695-KK, which is
XX given in an example from the present invention.
XX
XX Sequence 697 AA:

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```

Query Match 99.8%; Score 3646; DB 23; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.7e-236;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAPQIAMFCGRLLNMHMVQNKQKWDSPGSK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAPQIAMFCGRLLNMHMVQNKQKWDSPGSK 60
QY 61 TCIDTKESILQYCOEYVPELOITNNVEANOPVTIONMCKRGKQCKTHPHFVPIRCLVG 120
DB 61 TCIDTKESILQYCOEYVPELOITNNVEANOPVTIONMCKRGKQCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQEMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQEMDVCETHLHWHHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSEKVVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSEKVVVEAEVEEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVPTTAASTPDAY 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVPTTAASTPDAY 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSOVMRWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSOVMRWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420

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QY 421 KYRAEQKDRQHTLKHFEHVRWDPKKAQOIRSOVMTHLRVIERMNSUSLLYNPAPA 480
 DB 421 KYRAEQKDRQHTLKHFEHVRWDPKKAQOIRSOVMTHLRVIERMNSUSLLYNPAPA 480
 QY 481 EEIQDEYDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTIKITVTELLPVNGEFSL 540
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 QY 541 DDLPQWHSFGADSPANTENEVEPVDARPAADRLTTRPGSGLTNKTETSEIVKMDAEF 600
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 QY 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
 DB 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
 QY 661 VEYDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 697
 DB 661 VEYDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 697

RESULT 15
 AAW19498
 ID AAW19498 standard: protein; 695 AA.
 XX
 AC AAW19498;
 XX
 DT 08-SEP-1997 (first entry)
 DE APP695 mutant A-beta-containing protein.
 KW Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein;
 KW APP.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 642
 FT /note= "Wild-type Val is preferably substituted by Pro"
 XX
 PN W09640896-AL.
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09857.
 XX
 PR 07-JUN-1995; 95US-0480653.
 XX
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 XX
 PI Games KD, McConlogue LC, Rydel RE, Schenk DB, Seubert PA;
 XX
 DR WPI: 1997-052309/05.
 XX
 PT Testing compounds for an effect on an Alzheimer's disease marker -
 PT uses non-human transgenic animals which can control expression of
 PT major forms of beta-amyloid precursor protein.
 XX
 PS Claim 23; Page -: i39pp; English.
 XX
 CC A novel method has been produced for testing compounds for an effect on
 CC Alzheimer's disease (AD) marker. The method involves administering
 CC the compound to be tested to a non-human transgenic mammal, or mammalian
 CC cells derived from the transgenic mammal, where the transgenic mammal
 CC has a nucleic acid construct stably incorporated into the genome which
 CC comprises a promoter for expression of the construct in a mammalian cell
 CC operably linked to a region encoding an A-beta-containing protein. The
 CC region is selected from DNA encoding the A-beta-containing protein
 CC consisting of all, or a contiguous portion of APP70, APP751 or APP695,
 CC or a mutant comprising a mutation in one or more of amino acids 649,
 CC 670, 671, 690, 692 and 717, which includes amino acids 672-714 of human
 CC beta-amyloid precursor protein (APP). The present sequence represents a
 CC mutant APP695 protein in which the codon encoding amino acid 717 is

CC mutated (see features table). The amino acid positions referred to in
 CC the specification are as they appear in APP770 (see AAW19457) i.e.
 CC position 717 represents position 642 in APP695, and 698 in APP751. The
 CC larger forms of APP (APP751, APP770) consist of APP695 plus one or two
 CC additional domains. The method also involves detecting or measuring the
 CC AD marker such that any difference between the marker in the transgenic
 CC animal, or mammalian cells derived from the transgenic mammal, to which
 CC the compound has not been administered, is observed, where an observed
 CC difference in the marker indicates that the compound has an effect on
 CC the marker. The transgenic animals, or cells are used to screen for
 CC compounds which alter the pathological course of AD as measured by their
 CC effect on the amount and/or histopathology of AD markers in animals as
 CC well as behavioural alterations.
 CC N.B. The present sequence is shown in the specification, but has
 CC been derived from SEQ ID NO:2 which is on pages 103-105.
 XX
 SQ Sequence 695 AA:
 Query Match: 99.7%; Score 3643; DB 18; Length 695;
 Best Local Similarity 100.0%; Pred. No. 4,4e-256;
 Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MLPLGALLLLAAMTARALEVFTDGNAGLLAEPLQIAMFCGRNLNMHNVQNGKWDSPSGTK 60
 QY 61 TCIDTREGILQYCCVYPELOITNVVEANQPVTIONMCKGRKOCKTHPHFVLPYRCLVG 120
 DB 61 TCIDTREGILQYCCVYPELOITNVVEANQPVTIONMCKGRKOCKTHPHFVLPYRCLVG 120
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 DB 121 EFVSDALLVPDKCKELHOERHMDVCETHLHWHTVAKETCSKSTNLDYGMLLPGGDKPR 180
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 DB 181 GFVFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEEATERTTISIATITTTTETSEVEEVVYVTTAASPDVAV 300
 DB 241 EADDDDEDDGDEVEEAEPEEATERTTISIATITTTTETSEVEEVVYVTTAASPDVAV 300
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 DB 301 DKYLETPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEQAKNLPKADKKAVIQHF 360
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 DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
 QY 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQOIRSOVMTHLRVIERMNSUSLLYNPAPA 480
 DB 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQOIRSOVMTHLRVIERMNSUSLLYNPAPA 480
 QY 481 EEIQDEYDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTIKITVTELLPVNGEFSL 540
 DB 481 EEIQDEYDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTIKITVTELLPVNGEFSL 540
 QY 541 DDLPQWHSFGADSPANTENEVEPVDARPAADRLTTRPGSGLTNKTETSEIVKMDAEF 600
 DB 541 DDLPQWHSFGADSPANTENEVEPVDARPAADRLTTRPGSGLTNKTETSEIVKMDAEF 600
 QY 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
 DB 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
 QY 661 VEYDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 695
 DB 661 VEYDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 695

Search completed: October 2, 2003, 13:59:01
 Job time : 40.3333 secs

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OK protein - protein search, using sw model

Run on: October 2, 2003, 13:56:59 ; Search time 18 Seconds
(without alignments)
1638.370 Million cell updates/sec

Title: US-09-806-194-20

Perfect score: 3653

Sequence: 1 MLPGLALLLAANTARALEV.....QNGYENPTVKFFEQMNKK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310958 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pup.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3653	100.0	697	4	US-09-548-372D-20 Sequence 20, Appl
2	3653	100.0	697	4	US-09-548-367D-20 Sequence 20, Appl
3	3653	100.0	697	4	US-09-551-853D-20 Sequence 20, Appl
4	3646	99.8	697	4	US-09-548-372D-16 Sequence 16, Appl
5	3646	99.8	697	4	US-09-548-367D-16 Sequence 16, Appl
6	3646	99.8	697	4	US-09-551-853D-16 Sequence 16, Appl
7	3643	99.7	695	4	US-09-548-372D-14 Sequence 14, Appl
8	3643	99.7	695	4	US-09-548-367D-14 Sequence 14, Appl
9	3638	99.6	697	4	US-09-551-853D-14 Sequence 14, Appl
10	3638	99.6	697	4	US-09-548-372D-13 Sequence 13, Appl
11	3638	99.6	697	4	US-09-548-367D-13 Sequence 13, Appl
12	3638	99.6	697	4	US-09-551-853D-13 Sequence 13, Appl
13	3636	99.5	695	1	US-08-123-702-2 Sequence 2, Appl
14	3636	99.5	695	2	US-08-104-165-1 Sequence 1, Appl
15	3636	99.5	695	3	US-08-464-250-1 Sequence 1, Appl
16	3636	99.5	695	4	US-08-464-250-1 Sequence 7, Appl
17	3636	99.5	695	4	US-09-458-481B-7 Sequence 8, Appl
18	3636	99.5	695	4	US-09-458-481B-9 Sequence 10, Appl
19	3636	99.5	695	4	US-09-548-372D-10 Sequence 10, Appl
20	3636	99.5	695	4	US-09-548-367D-10 Sequence 10, Appl
21	3636	99.5	695	4	US-09-551-853D-10 Sequence 10, Appl
22	3636	99.5	695	6	5218100-2 Patent No. 5218100
23	3630	99.4	694	1	US-08-339-52A-18 Sequence 18, Appl
24	3630	99.4	694	2	US-08-007-996B-5 Sequence 5, Appl
25	3630	99.4	694	2	US-08-689-276A-5 Sequence 5, Appl
26	3628	99.3	695	4	US-09-548-372D-12 Sequence 12, Appl
27	3628	99.3	695	4	US-09-548-367D-12 Sequence 12, Appl

28 3628 99.3 695 4 US-09-551-853D-12 Sequence 12, Appl

29 3624 99.2 695 1 US-08-371-930-27 Sequence 27, Appl

30 3624 99.2 695 5 PCT-US94-01712-27 Sequence 27, Appl

31 3612 98.9 695 1 US-08-339-152A-30 Sequence 30, Appl

32 3607 98.7 753 4 US-09-548-372D-61 Sequence 61, Appl

33 3607 98.7 753 4 US-09-548-367D-61 Sequence 61, Appl

34 3607 98.7 753 4 US-09-551-853D-61 Sequence 61, Appl

35 3597 98.5 751 1 US-08-123-702-4 Sequence 4, Appl

36 3597 98.5 751 2 US-08-104-165-2 Sequence 2, Appl

37 3597 98.5 751 2 US-08-422-333-2 Sequence 2, Appl

38 3597 98.5 751 3 US-08-422-333-21 Sequence 21, Appl

39 3597 98.5 751 3 US-08-464-250-2 Sequence 2, Appl

40 3597 98.5 751 4 US-08-464-250-2 Sequence 2, Appl

41 3597 98.5 751 4 US-08-832-667-5 Sequence 5, Appl

42 3597 98.5 751 4 US-09-548-372D-57 Sequence 57, Appl

43 3597 98.5 751 4 US-09-548-367D-57 Sequence 57, Appl

44 3597 98.5 751 4 US-09-551-853D-57 Sequence 57, Appl

45 3597 98.5 751 6 5187153-2 Patent No. 5187153

ALIGNMENTS

RESULT 1

US-09-548-372D-20

: Sequence 20, Application US/09548372D

: Patent No. 6420534

: GENERAL INFORMATION:

: APPLICANT: GURNEY ET AL.

: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND

: TITLE OF INVENTION: THEREOF

: FILE REFERENCE: 29915/62801

: CURRENT APPLICATION NUMBER: US/09/548,372D

: CURRENT FILING DATE: 2000-04-12

: PRIOR APPLICATION NUMBER: US 60/155,493

: PRIOR FILING DATE: 1999-09-23

: PRIOR APPLICATION NUMBER: US 09/404,133

: PRIOR FILING DATE: 1999-09-23

: PRIOR APPLICATION NUMBER: PCT/US95/20881

: PRIOR FILING DATE: 1999-09-23

: PRIOR APPLICATION NUMBER: US 60/101,594

: PRIOR FILING DATE: 1998-09-24

: NUMBER OF SEQ ID NOS: 73

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 20

: LENGTH: 697

: TYPE: PRT

: ORGANISM: Homo sapiens

US-09-548-372D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;

Best Local Similarity 100.0%; Pred. No. 4.9e-265;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHVMVQNGKWDSPSGTK 60

Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHVMVQNGKWDSPSGTK 60

Qy 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIQNCKRGRKQCKTHPHFVTPYRCLVG 120

Db 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIQNCKRGRKQCKTHPHFVTPYRCLVG 120

Qy 121 EFVSDALLVDEKCKFLHOERMDVCETHLHWHHTYAKETCSEKSTNLDHYGMLLPCGTDKFR 180

Db 121 EFVSDALLVDEKCKFLHOERMDVCETHLHWHHTYAKETCSEKSTNLDHYGMLLPCGTDKFR 180

Qy 181 GFVFVCCPLAEESDNVDSADAEDDDSDVMWGGADTYADGSEDKVVEAEVEAEVEE 240

Db 181 GFVFVCCPLAEESDNVDSADAEDDDSDVMWGGADTYADGSEDKVVEAEVEAEVEE 240

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Db 241 EADDDDEDDGDEVEEAEPYEATERTTISIATTTTTITTESVEEYVRVPTTAASPDV 300

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DB 301 DKYLETGPDNEHAHFQKAKERLEAKHREMSQVMREKEAECAQKSLPKADKKAVIQHF 360
QY 361 GEKVESLEQEAANEERQOLVETHMARVEAMINDRRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 GEKVESLEQEAANEERQOLVETHMARVEAMINDRRRLALENYITALQAVPPRPHVFNMLK 420
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DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVA 480
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DB 481 EBIQDEVDELLQKEQNSDQVLANMISEPRISYGNDAIMPSTETTKTTVELLPVNGEESL 540
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DB 541 DDLOPHSFAGADSVDPANTEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGGV 660
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DB 661 VEYDAAVTPEERHLSKMQONGYENPTYKPFQOMONKK 697

RESULT 2
US-09-548-367D-20
: Sequence 20, Application US/09548367D
: Patent No. 6440598
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: THEREOF
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 29915/6280H
: CURRENT APPLICATION NUMBER: US/09/548,367D
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-548-367D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 4,9e-265;
Matches 697; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TCIDTKEGILQYCOEVYPELQITNVNEANQPTIQNWCKRGRKCKTHPHEVIPYRCLVG 120
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DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHYVAKETCSSEKSTNLHUYGMLLPCGIDKFR 180
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DB 361 QKVESLEQEAANEERQOLVETHMARVEAMINDRRRLALENYITALQAVPPRPHVFNMLK 420
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QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKPFQOMONKK 697
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RESULT 3
US-09-551-853D-20
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: Patent No. 6500667
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 29915/6280C
: CURRENT APPLICATION NUMBER: US/09/551,853D
: PRIOR FILING DATE: 2000-04-18
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-551-853D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 4,9e-265;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLIAEPOIAMFCGRLNHMHNVONGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLIAEPOIAMFCGRLNHMHNVONGKWDSPSGTK 60
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QY      181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADIDYADGSEKRVVEAEVEAEVEAEVEE 240
Db      181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADIDYADGSEKRVVEAEVEAEVEAEVEE 240
QY      241 EADDDDDDDGDEVEAEPEEATERTTSTATTTTTSVEEVVVRVPTTAASPTDAV 300
Db      241 EADDDDDDDGDEVEAEPEEATERTTSTATTTTTSVEEVVVRVPTTAASPTDAV 300
QY      301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAEQAKNLPKADKKAIVQHF 360
Db      301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAEQAKNLPKADKKAIVQHF 360
QY      361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db      361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY      421 KYVRAEKORQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSQLLYNVPVAV 480
Db      421 KYVRAEKORQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSQLLYNVPVAV 480
QY      481 EETQDEVEDELLOKEQNSQCVLANMISEPRISYGNDAIMPSTETKTIVELLVPNGEFSL 540
Db      481 EETQDEVEDELLOKEQNSQCVLANMISEPRISYGNDAIMPSTETKTIVELLVPNGEFSL 540
QY      541 DLQPMSEFGADSVDPANTENEPVDARPAADRGLTIRPGSGLTINIKTEISEVKMDAEF 600
Db      541 DLQPMSEFGADSVDPANTENEPVDARPAADRGLTIRPGSGLTINIKTEISEVKMDAEF 600
QY      601 RHDSCYEVHHQKLVFFAEADVGSNKGAIGLWVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
Db      601 RHDSCYEVHHQKLVFFAEADVGSNKGAIGLWVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
QY      661 VEYDAAVTPERHLSKMOQNGYENPTYKFFEQMNKK 697
Db      661 VEYDAAVTPERHLSKMOQNGYENPTYKFFEQMNKK 697
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RESULT 4

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US-09-548-372D-16
; Sequence 16, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 69/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-16
```

Query Match 99.8%; Score 3646; DB 4; Length 697;
Best Local Similarity 99.9%; Pred. No. 1.6e-264;

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Matches 69%; Conservative G; Mismatches 1; Indels 0; Gaps 0;
QY      1 MLPGLALLLLAAWTARALEVPTDGNAGLAEPQIAMFCGRLNHHMNQVNGKWDSDPSGTK 60
Db      1 MLPGLALLLLAAWTARALEVPTDGNAGLAEPQIAMFCGRLNHHMNQVNGKWDSDPSGTK 60
QY      61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONWCKRGKCKTHPHFV1PYRCLVG 120
Db      61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONWCKRGKCKTHPHFV1PYRCLVG 120
QY      121 EFVSDALLVPDKCKFLHQRMDVCEHRLHWHVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db      121 EFVSDALLVPDKCKFLHQRMDVCEHRLHWHVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY      181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADIDYADGSEKRVVEAEVEAEVEAEVEE 240
Db      181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADIDYADGSEKRVVEAEVEAEVEAEVEE 240
QY      241 EADDDDDDDGDEVEAEPEEATERTTSTATTTTTSVEEVVVRVPTTAASPTDAV 300
Db      241 EADDDDDDDGDEVEAEPEEATERTTSTATTTTTSVEEVVVRVPTTAASPTDAV 300
QY      301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAEQAKNLPKADKKAIVQHF 360
Db      301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAEQAKNLPKADKKAIVQHF 360
QY      361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db      361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY      421 KYVRAEKORQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSQLLYNVPVAV 480
Db      421 KYVRAEKORQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSQLLYNVPVAV 480
QY      481 EETQDEVEDELLOKEQNSQCVLANMISEPRISYGNDAIMPSTETKTIVELLVPNGEFSL 540
Db      481 EETQDEVEDELLOKEQNSQCVLANMISEPRISYGNDAIMPSTETKTIVELLVPNGEFSL 540
QY      541 DLQPMSEFGADSVDPANTENEPVDARPAADRGLTIRPGSGLTINIKTEISEVKMDAEF 600
Db      541 DLQPMSEFGADSVDPANTENEPVDARPAADRGLTIRPGSGLTINIKTEISEVKMDAEF 600
QY      601 RHDSCYEVHHQKLVFFAEADVGSNKGAIGLWVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
Db      601 RHDSCYEVHHQKLVFFAEADVGSNKGAIGLWVGGVVIATVIFITLVMLKKKQYTSIHGGV 660
QY      661 VEYDAAVTPERHLSKMOQNGYENPTYKFFEQMNKK 697
Db      661 VEYDAAVTPERHLSKMOQNGYENPTYKFFEQMNKK 697
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RESULT 5

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US-09-548-367D-16
; Sequence 16, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
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; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-16

Query Match          99.83; Score 3646; DB 4; Length 697;
Best Local Similarity 99.94; Pred. No. 1.6e-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPTQAMFCGRINMHMNVQNGKWDSDPSGK 60
DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPTQAMFCGRINMHMNVQNGKWDSDPSGK 60

QY 61 TCIDTKGILQYCOEYVPELQITNVVEANQPTVIONCKKGRKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKGILQYCOEYVPELQITNVVEANQPTVIONCKKGRKCKTHPHFVPIYRCVLG 120

QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240

QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVEVVPVTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVEVVPVTTAASTPDV 300

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAKNLPKADKKAVIQHF 360

QY 361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITLQAVPPRPRHVFNMKL 420
DB 361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITLQAVPPRPRHVFNMKL 420

QY 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
DB 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480

QY 481 ESIQDEVDLLOKQFQNYSDVLANMISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540
DB 481 ESIQDEVDLLOKQFQNYSDVLANMISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540

QY 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGTLTPGSLNIKTEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGTLTPGSLNIKTEISEVKMDAEF 600

QY 601 RHDSGYEVHHQKLVPFAEDVGSNKGATIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVPFAEDVGSNKGATIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660

QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 6
US-09-551-853D-16
; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551.853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn: version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-16

Query Match          99.84; Score 3646; DB 4; Length 697;
Best Local Similarity 99.94; Pred. No. 1.6e-264;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPTQAMFCGRINMHMNVQNGKWDSDPSGK 60
DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPTQAMFCGRINMHMNVQNGKWDSDPSGK 60

QY 61 TCIDTKGILQYCOEYVPELQITNVVEANQPTVIONCKKGRKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKGILQYCOEYVPELQITNVVEANQPTVIONCKKGRKCKTHPHFVPIYRCVLG 120

QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240

QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVEVVPVTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVEVVPVTTAASTPDV 300

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEAKNLPKADKKAVIQHF 360

QY 361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITLQAVPPRPRHVFNMKL 420
DB 361 QKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITLQAVPPRPRHVFNMKL 420

QY 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
DB 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480

QY 481 ESIQDEVDLLOKQFQNYSDVLANMISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540
DB 481 ESIQDEVDLLOKQFQNYSDVLANMISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540

QY 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGTLTPGSLNIKTEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGTLTPGSLNIKTEISEVKMDAEF 600

QY 601 RHDSGYEVHHQKLVPFAEDVGSNKGATIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVPFAEDVGSNKGATIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660

QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 7
US-09-548-372D-14
; Sequence 14, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND I
; TITLE OF INVENTION: THEREOF

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Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQTRSQVM:HLRVIERMNSLSLLYNVPAVA 480
|||||
Qy 481 EEOQDEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSSLFTKTTIVELLPVNGEESL 540
|||||
Db 481 EEOQDEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSSLFTKTTIVELLPVNGEESL 540
|||||
Qy 541 DDLQPHWSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKKMADEF 600
|||||
Db 541 DDLQPHWSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVNLDAEF 600
|||||
Qy 601 RHDSGYEVHHOKLVFFAEDVCSNKGAIGLVMGVVATVIF:TLVNLKKKKOYTSIHHGV 660
|||||
Db 601 RHDSGYEVHHOKLVFFAEDVCSNKGAIGLVMGVVATVIV:TLVNLKKKKOYTSIHHGV 660
|||||
Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
|||||
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
|||||

RESULT 11
US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/628CH
; CURRENT APPLICATION NUMBER: US/09/548.367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-18

Query Match 99.6%; Score 3638; DB 4; Length 697;
Best Local Similarity 99.6%; Pred. No. 6.4e-264;
Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVQNGKWDSPSGTK 60
|||||
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVQNGKWDSPSGTK 60
|||||
Qy 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONCKRGRKCK*HPIHFVPIYRCLVG 120
|||||
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONCKRGRKCKTHPIHFVPIYRCLVG 120
|||||
Qy 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|||||
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|||||
Qy 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEEVEE 240
|||||
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEEVEE 240
|||||
Qy 241 EADDEDEDCDEVEEAEPEEATERTTSIATTTTITESVEEVVRPITAASTPDVA 300
|||||
Db 241 EADDEDEDCDEVEEAEPEEATERTTSIATTTTITESVEEVVRPITAASTPDVA 300
|||||
Qy 301 DKYLETPGDENEHAHQKAKERLEAKHRRKMSQVREWEAEERQAKNLPKADKAVIOHF 360
|||||
```

```
Db 301 DKYLETPGDENEHAHQKAKERLEAKHRRKMSQVREWEAEERQAKNLPKADKAVIOHF 360
|||||
Qy 361 QEKVESLEOEAAEROLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMILK 420
|||||
Db 361 QEKVESLEOEAAEROLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMILK 420
|||||
Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNVPAVA 480
|||||
Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNVPAVA 480
|||||
Qy 481 EEOQDEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSSLFTKTTIVELLPVNGEESL 540
|||||
Db 481 EEOQDEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSSLFTKTTIVELLPVNGEESL 540
|||||
Qy 541 DDLQPHWSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKKMADEF 600
|||||
Db 541 DDLQPHWSFGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVNLDAEF 600
|||||
Qy 601 RHDSGYEVHHOKLVFFAEDVCSNKGAIGLVMGVVATVIF:TLVNLKKKKOYTSIHHGV 660
|||||
Db 601 RHDSGYEVHHOKLVFFAEDVCSNKGAIGLVMGVVATVIV:TLVNLKKKKOYTSIHHGV 660
|||||
Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
|||||
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
|||||

RESULT 12
US-09-551-853D-18
; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-18

Query Match 99.6%; Score 3638; DB 4; Length 697;
Best Local Similarity 99.6%; Pred. No. 6.4e-264;
Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVQNGKWDSPSGTK 60
|||||
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHNVQNGKWDSPSGTK 60
|||||
Qy 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONCKRGRKCKTHPIHFVPIYRCLVG 120
|||||
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONCKRGRKCKTHPIHFVPIYRCLVG 120
|||||
Qy 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|||||
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|||||
Qy 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEEVEE 240
|||||
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEEVEE 240
|||||
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QY 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTTSVEEVRVPTAASTPDAY 300
DB 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTTSVEEVRVPTAASTPDAY 300
QY 301 DKYLETPGDNFHAHFOKAKERLEAKHRERMSOVHKEWFEAEKQAKNPKADPKAVIQHP 360
DB 301 DKYLETPGDNFHAHFOKAKERLEAKHRERMSOVHKEWFEAEKQAKNPKADPKAVIQHP 360
QY 361 QEVESLEOEAANERQOLVETHMARVEAMNDRRLALENYITATGAVPPRPHVFNMLK 420
DB 361 QEVESLEOEAANERQOLVETHMARVEAMNDRRLALENYITATGAVPPRPHVFNMLK 420
QY 421 KYVRAEOKDROHTLKHFHFVRMVDPKKAAQIRSOVMTHLRVIVERNQSLSLLYNYPAVA 480
DB 421 KYVRAEOKDROHTLKHFHFVRMVDPKKAAQIRSOVMTHLRVIVERNQSLSLLYNYPAVA 480
QY 481 BEIODEVDELLQEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELPVGNEFSL 540
DB 481 BEIODEVDELLQEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELPVGNEFSL 540
QY 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKNDAEF 600
DB 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKNDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVATVITVLMLKKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVATVITVLMLKKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQQNGYENPTYKFFEQMONKK 697
DB 661 VEYDAAVTPEERHLSKMQQNGYENPTYKFFEQMONKK 697

RESULT 13
US-08-123-702-2
; Sequence 2, Application US/08123702
; Patent No. 5604131
; GENERAL INFORMATION:
; APPLICANT: Wadsworth, Samuel
; APPLICANT: Snyder, Benjamin
; APPLICANT: Reddy, Vermur, B.
; APPLICANT: Wei, Chamar
; TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770
; Patent No. 5604131
; TITLE OF INVENTION: Containing a Genomic DNA Insert of the K1 and Cx-2 Regions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123.702
; FILING DATE: 17-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,264
; REFERENCE/DOCKET NUMBER: TS1121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 695 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-702-2

Query Match
Best Local Similarity 99.9%; Score 3636; DB 1: Length 695;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TCIDTKEGIIQYCOEVPYELQITNVYFANOPVTIONCKKGRKQCKTHPIHFVPIYPCLVG 120
DB 61 TCIDTKEGIIQYCOEVPYELQITNVYFANOPVTIONCKKGRKQCKTHPIHFVPIYPCLVG 120
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QY 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTTSVEEVRVPTAASTPDAY 300
DB 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTTSVEEVRVPTAASTPDAY 300
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DB 301 DKYLETPGDNFHAHFOKAKERLEAKHRERMSOVHKEWFEAEKQAKNPKADPKAVIQHP 360
QY 361 QEVESLEOEAANERQOLVETHMARVEAMNDRRLALENYITATGAVPPRPHVFNMLK 420
DB 361 QEVESLEOEAANERQOLVETHMARVEAMNDRRLALENYITATGAVPPRPHVFNMLK 420
QY 421 KYVRAEOKDROHTLKHFHFVRMVDPKKAAQIRSOVMTHLRVIVERNQSLSLLYNYPAVA 480
DB 421 KYVRAEOKDROHTLKHFHFVRMVDPKKAAQIRSOVMTHLRVIVERNQSLSLLYNYPAVA 480
QY 481 BEIODEVDELLQEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELPVGNEFSL 540
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QY 661 VEYDAAVTPEERHLSKMQQNGYENPTYKFFEQMON 695
DB 661 VEYDAAVTPEERHLSKMQQNGYENPTYKFFEQMON 695

RESULT 14
US-08 104-365-1
; Sequence 1, Application US/08104165
; Patent No. 5877015
; GENERAL INFORMATION:
; APPLICANT: HARDY, John Anthony
; APPLICANT: GOATE, Alison Mary
; APPLICANT: MULLAN, Michael John
; APPLICANT: CHARTIER-HARLIN, Marie-Christine
; APPLICANT: OWEN, Michael John
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew

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: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: OPERATING SYSTEM: IBM PC compatible
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/104.165
: FILING DATE: 21-JAN-1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 910307.8
: FILING DATE: 21-JAN-1992
: APPLICATION NUMBER: 9118445.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-104-165-1

Query Match 99.5%; Score 3636; DB 3; Length 695;
Best Local Similarity 99.9%; Pred. No. 9e-264;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 EFVSDALVPDKKFLHQRMDVCGETHLHHHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
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DB 361 QEKVESLEQEAANERQQLVETIHARVEAMLDNRRLALENYITLQAVPFRPRVFNMLK 420
QY 421 KYVRAEQDRGHTLKHFHEVRWMDPKKAAQIRSOVMTHLRVIYERMQS:SLLYNVPAVA 480
DB 421 KYVRAEQDRGHTLKHFHEVRWMDPKKAAQIRSOVMTHLRVIYERMQS:SLLYNVPAVA 480
QY 481 EETQDEVDELLOKQNSLOVLIANNISEPRIYSYNDALMPSLTETKTVELLPYNGEFSL 540
DB 481 EETQDEVDELLOKQNSLOVLIANNISEPRIYSYNDALMPSLTETKTVELLPYNGEFSL 540

: STREETS: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: OPERATING SYSTEM: IBM PC compatible
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/104.165
: FILING DATE: 21-JAN-1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 910307.8
: FILING DATE: 21-JAN-1992
: APPLICATION NUMBER: 9118445.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-104-165-1

: Sequence 1, Application US/08/104.165
: Patent No. 6,075,422
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: GOATE, Alison Mary
: APPLICANT: MULLAN, Michael John
: APPLICANT: CHARLIER-HARLIN, Marie-Christine
: APPLICANT: OWEN, Michael John
: TITLE OF INVENTION: Test and Model for Alzheimer's Disease
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Hourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: OPERATING SYSTEM: IBM PC compatible
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/104.165
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/104,165
: FILING DATE: 21-JAN-1992
: APPLICATION NUMBER: 910307.8
: FILING DATE: 21-JAN-1991
: APPLICATION NUMBER: 9118445.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-104-165-1

Query Match 99.5%; Score 3636; DB 3; Length 695;
Best Local Similarity 99.9%; Pred. No. 9e-264;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      601 RHDSCGYEVHHOKLVFFAEDEVGSNKGATIGLMVGCVIATVITLVMKKKQYTSIHGV 660
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Search completed: October 2, 2003, 14:03:38
 Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compaden Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 14:00:39 ; Search time 39 Seconds
(without alignments);
2827.550 Million cell updates/sec

Title: US-09-806-194-20

Perfect score: 3653

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 597654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 567654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	3653	100.0	697	9	US-09-794-748-20
5	3653	100.0	697	9	US-09-794-925-20
6	3653	100.0	697	9	US-09-681-442-20
7	3653	100.0	697	11	US-09-869-414-20
8	3653	100.0	697	9	US-09-548-366-20
9	3646	99.8	697	9	US-09-794-927-16
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11	3646	99.8	697	9	US-09-794-743-16
12	3646	99.8	697	9	US-09-794-748-16
13	3646	99.8	697	9	US-09-794-925-16
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18	3643	99.7	695	9	US-09-795-847-14
19	3643	99.7	695	9	US-09-794-743-14
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ALIGNMENTS

RESULT 1

US-09-794-927-20
: Sequence 20, Application US/09794927
: Patent No. US20010016324A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AT
: TITLE OF INVENTION: USES
: FILE REFERENCE: 28341/5280FG
: CURRENT APPLICATION NUMBER: US/09/794,927
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patent in Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens

Query Match 100.0%; Score 3653; DB 9; Length 697;

Best Local Similarity 100.0%; Pred. No. 2,1e-226;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAFMFCGRLNMHMVQNGKWSOPSGTK 60
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DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSLTNKITEISEVKMDAEF 600
QY 601 RHDGSEVHHQKLVFAEDVGSNGKGAIIGLMVGGVVIAVIFITLVMKKQYTSIHGV 660
DB 601 RHDGSEVHHQKLVFAEDVGSNGKGAIIGLMVGGVVIAVIFITLVMKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697

RESULT 2
US-09-795-847-20
: Sequence 20, Application: US/09795847
: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USFS
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/62800E
: CURRENT APPLICATION NUMBER: US/09/795,847
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23

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: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-795-847-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAFMFCGRLNMHMVQNGKWSOPSGTK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAFMFCGRLNMHMVQNGKWSOPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVITQNWCKRGKCKTHPHFVIPPYCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVITQNWCKRGKCKTHPHFVIPPYCLVG 120
QY 121 EFVSDALLVPDKCFKHQERMDVCETHLHWHHTVAKETCSKSTNLHDYGMILPCGIDKFR 180
DB 121 EFVSDALLVPDKCFKHQERMDVCETHLHWHHTVAKETCSKSTNLHDYGMILPCGIDKFR 180
QY 181 GVFEVCCPLAESDNVDSADAEEDSDVMWKGADIDYAGSSEDKVVEAEVEEVAEVEE 240
DB 181 GVFEVCCPLAESDNVDSADAEEDSDVMWKGADIDYAGSSEDKVVEAEVEEVAEVEE 240
QY 241 EADDEDEDGDEVEEAEPEEATERTTSIAITTTTTSVEEVRVPTTAASPTDAV 300
DB 241 EADDEDEDGDEVEEAEPEEATERTTSIAITTTTTSVEEVRVPTTAASPTDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITAJQAVPRPRHVFNMKL 420
DB 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITAJQAVPRPRHVFNMKL 420
QY 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLLYNYPAVA 480
DB 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLLYNYPAVA 480
QY 481 EEIQDEVDLQKEQYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFSL 540
DB 481 EEIQDEVDLQKEQYSDVLANMISEPRISYGNDAIMPSTETKTITVELLPVNGEFSL 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSLTNKITEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSLTNKITEISEVKMDAEF 600
QY 601 RHDGSEVHHQKLVFAEDVGSNGKGAIIGLMVGGVVIAVIFITLVMKKQYTSIHGV 660
DB 601 RHDGSEVHHQKLVFAEDVGSNGKGAIIGLMVGGVVIAVIFITLVMKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPEERHLSKMOQNGYENPTYKFFEQMNKK 697

RESULT 3
US-09-794-743-20
: Sequence 20, Application: US/09794743
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang

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: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: US95
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280BC
: CURRENT FILING DATE: 2001-02-27
: PRIOR FILING DATE: 2001-02-27
: PRIOR FILING DATE: 1999-10-13
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRI
: ORGANISM: Homo sapiens
US-09-794-743-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2,1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNLNMMNVQNGKWSDDPSGTK 60
D 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNLNMMNVQNGKWSDDPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKGRKQCKTHPHFVPIYRCLVG 120
D 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKGRKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPCGIDKER 180
D 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPCGIDKER 180
QY 181 GVEFVCCPLAESNDVSDADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEEVEE 240
D 181 GVEFVCCPLAESNDVSDADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRVPTTAASPPDAV 300
D 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRVPTTAASPPDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMEKEEAEERQAKNLPKADKKAVIQHF 360
D 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMEKEEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMNDRRRLALENYITALQAVPPRPHVFNMLK 420
D 361 QEKVESLEQEAANERQOLVETHMARVEAMNDRRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQSLSLLYNPVAVA 480
D 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQSLSLLYNPVAVA 480
QY 661 VEVDAAVTPEERLSKMQQNGYENPTYKFFEQMONKK 697
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: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
: TITLE OF INVENTION: US95
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280JL
: CURRENT FILING DATE: 2001-02-27
: PRIOR FILING DATE: 2001-02-27
: PRIOR FILING DATE: 1999-10-13
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1999-09-23
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRI
: ORGANISM: Homo sapiens
US-09-794-748-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2,1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNLNMMNVQNGKWSDDPSGTK 60
D 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNLNMMNVQNGKWSDDPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKGRKQCKTHPHFVPIYRCLVG 120
D 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKGRKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPCGIDKER 180
D 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPCGIDKER 180
QY 181 GVEFVCCPLAESNDVSDADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEEVEE 240
D 181 GVEFVCCPLAESNDVSDADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRVPTTAASPPDAV 300
D 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRVPTTAASPPDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMEKEEAEERQAKNLPKADKKAVIQHF 360
D 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMEKEEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMNDRRRLALENYITALQAVPPRPHVFNMLK 420
D 361 QEKVESLEQEAANERQOLVETHMARVEAMNDRRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQSLSLLYNPVAVA 480
D 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQSLSLLYNPVAVA 480
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QY 481 EEIQEYDELLQKQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
DB 481 EETODEVELLQKQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
QY 541 DDLOPHSFGADSVDPANTEVEPVDPADPAADRGLTTRPGSGLTNKTETSEVKKMDAEF 600
DB 541 DDLOPHSFGADSVDPANTEVEPVDPADPAADRGLTTRPGSGLTNKTETSEVKKMDAEF 600
QY 601 RHDSSYEVHOKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYIS:HHGV 660
DB 601 RHDSSYEVHOKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYIS:HHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 5
US-09-794-925-20
; Sequence 20, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/6280H1
; CURRENT APPLICATION NUMBER: US/09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2,1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNHNNVQNGKWDSDSGTK 60
DB 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNHNNVQNGKWDSDSGTK 60
QY 61 TCIDTKEGILQYCVFVPELQITNNVVEANOPVTIQNMCKRGRKCKTHPRV:PYKCLVG 120
DB 61 TCIDTKEGILQYCVFVPELQITNNVVEANOPVTIQNMCKRGRKCKTHPRV:PYKCLVG 120
QY 121 LFVSDALLVPCKFLHQRNDVCEETHLHHVTAKECTSEKSNLHHDYGMJLJFCGGIDKFR 180
DB 121 LFVSDALLVPCKFLHQRNDVCEETHLHHVTAKECTSEKSNLHHDYGMJLJFCGGIDKFR 180
QY 181 GVEFFVCCPLAESDNVDSADAEEDSDVMMGADTDVADGSEDKVSVVAEEFEVAVEEER 240
DB 181 GVEFFVCCPLAESDNVDSADAEEDSDVMMGADTDVADGSEDKVSVVAEEFEVAVEEER 240
QY 241 EADDDEDDDEGDEVEEAEPEEATEKTTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300
DB 241 EADDDEDDDEGDEVEEAEPEEATEKTTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300
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DB 241 EADDDEDDDEGDEVEEAEPEEATEKTTTSIATTTTTTIESVEEVVRVPTTAASTPDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQBAANRQOLVETHMARVEMLUNDRRR:ALENYITAIQAVIPRPHVFNMLK 420
DB 361 QEKVESLEQBAANRQOLVETHMARVEMLUNDRRR:ALENYITAIQAVIPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIERMNQSLSLLYNPVAV 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIERMNQSLSLLYNPVAV 480
QY 481 BEIQDEVELLQKQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
DB 481 BEIQDEVELLQKQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
QY 541 DDLOPHSFGADSVDPANTEVEPVDPADPAADRGLTTRPGSGLTNKTETSEVKKMDAEF 600
DB 541 DDLOPHSFGADSVDPANTEVEPVDPADPAADRGLTTRPGSGLTNKTETSEVKKMDAEF 600
QY 601 RHDSSYEVHOKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYIS:HHGV 660
DB 601 RHDSSYEVHOKLVFFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYIS:HHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 6
US-09-681-442-20
; Sequence 20, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2,1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNHNNVQNGKWDSDSGTK 60
DB 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNHNNVQNGKWDSDSGTK 60
QY 61 TCIDTKEGILQYCVFVPELQITNNVVEANOPVTIQNMCKRGRKCKTHPRV:PYKCLVG 120
DB 61 TCIDTKEGILQYCVFVPELQITNNVVEANOPVTIQNMCKRGRKCKTHPRV:PYKCLVG 120
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Db	61	TCIDTKEGTQYQCQVYDELOITNVVEANQPVITONWCKRGKQCKTHPHFVTPYECVGL	120
Qy	121	EFVSDALLVPDKCKFLHGERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPCGIDKXFR	180
Db	121	EFVSDALLVPDKCKFLHGERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPCGIDKXFR	180
Qy	181	GVFEVCCPLAESDNVDSADAEODSDVWVGADTYADGSEDKVVEVAEEHVAEVESE	240
Db	181	GVFEVCCPLAESDNVDSADAEODSDVWVGADTYADGSEDKVVEVAEEHVAEVESE	240
Qy	241	EADDDDEDDGDEVEEEAEPEYEAETPTTSIATITITITTESVEEVVVPVPTTAAS*PDVA	300
Db	241	EADDDDEDDGDEVEEEAEPEYEAETPTTSIATITITTESVEEVVVPVPTTAAS*PDVA	300
Qy	301	DKYLETPGDENEHAFQAKERLEAKHPRMSQVMREWEAEAEQAOKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAFQAKERLEAKHPRMSQVMREWEAEAEQAOKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPVRPRHVENMLK	420
Db	361	QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPVRPRHVENMLK	420
Qy	421	KYVRAEQDKRQHTLKHFSHVHRWDPFKAAQITRSQVMTHLRVIVERNMQSLSLNYNPAVA	480
Db	421	KYVRAEQDKRQHTLKHFSHVHRWDPFKAAQITRSQVMTHLRVIVERNMQSLSLNYNPAVA	480
Qy	481	EIEIQEVDDELQKEQNYSDDVLANMISEPRISYNDALMPSLETITKTVELLPVNGEFSL	540
Db	481	EIEIQEVDDELQKEQNYSDDVLANMISEPRISYNDALMPSLETITKTVELLPVNGEFSL	540
Qy	541	DLQVPHSFGADSVPAENTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEVKMDAEF	600
Db	541	DLQVPHSFGADSVPAENTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFFAEDVGSNGKAIIGLVMVGWVIATVIFITLVMLKKQVTSIHGV	660
Db	601	RHDSGYEVHHQKLVFFAEDVGSNGKAIIGLVMVGWVIATVIFITLVMLKKQVTSIHGV	660
Qy	661	VEYDAAVTPDERHLSKMOONGYENPTYKFFEQMONKK	697
Db	661	VEYDAAVTPDERHLSKMOONGYENPTYKFFEQMONKK	697

RESULT 7
US-09-869-414-20
; Sequence 20, Application US/09869414
; Publication No. US20030077226A1
; GENERAL INFORMATION:
; APPLICANT: Beinowski et al.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280M
; CURRENT APPLICATION NUMBER: US/09/869,414
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-869-414-20

RESULT 8
US-09-548-366-20
; Sequence 20, Application US/09548366
; Publication No. US20030104365A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yao, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-366-20

Query Match      100.0%; Score 3653; DB 11; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAIFCGRLNMHNMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAIFCGRLNMHNMVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVPIRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETCEKSTNLHDYGMLLPCGIDKPR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETCEKSTNLHDYGMLLPCGIDKPR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIAITTTTIESVEEVVVPVPTTAASPTDAV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIAITTTTIESVEEVVVPVPTTAASPTDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVENMLK 420
DB 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVA 480
QY 481 FEIQDEVDLLOKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540
DB 481 FEIQDEVDLLOKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660

; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-16

Query Match      99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.8%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAIFCGRLNMHNMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAIFCGRLNMHNMVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVPIRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETCEKSTNLHDYGMLLPCGIDKPR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETCEKSTNLHDYGMLLPCGIDKPR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIAITTTTIESVEEVVVPVPTTAASPTDAV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIAITTTTIESVEEVVVPVPTTAASPTDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVENMLK 420
DB 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVA 480
QY 481 FEIQDEVDLLOKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540
DB 481 FEIQDEVDLLOKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
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RESULT 9

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US-09-794-927-16
; Sequence 16, Application US/09/794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
```

QY 661 VEYDAVTPERHLSKMOONGYENPTYKFFEQMONKK 657
Db 661 VEYDAVTPERHLSKMOONGYENPTYKFFEQMONKK 657

RESULT 10
US-09-795-847-16
: Sequence 16, Application US/09795847
: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280DF
: CURRENT APPLICATION NUMBER: US/09/795,847
: CURRENT FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-795-847-16

Query Match 99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNYQNGKWDSPSGTK 60
Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNYQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSECKVVEVAEEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSECKVVEVAEEVEE 240
QY 241 EADDEDEDEDEVEEAEPEEATENTTSIATTTTIESVEEVKVPPTAASTPDV 300
Db 241 EADDEDEDEDEVEEAEPEEATENTTSIATTTTIESVEEVKVPPTAASTPDV 300
QY 301 DKYLETPGDENEHAHFOKAKERLEAKHRMSQVNRWEAEERAKNLPKADKKAIVQHF 360
Db 301 DKYLETPGDENEHAHFOKAKERLEAKHRMSQVNRWEAEERAKNLPKADKKAIVQHF 360
QY 361 QEKVESLQEAANERQOIVETHMARVEAMLNDRRLALENTITALQVPPRPREFVFNMLK 420
Db 361 QEKVESLQEAANERQOIVETHMARVEAMLNDRRLALENTITALQVPPRPREFVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTLRLVIERMNQSLSLLYNPAVA 480

Db 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTLRLVIERMNQSLSLLYNPAVA 480
QY 481 EEIQDEVDLQKEQNYSDVLAMNISEPRISYGNDAJLMPSLIETKTIVELLPVNGEFSL 540
Db 481 EEIQDEVDLQKEQNYSDVLAMNISEPRISYGNDAJLMPSLIETKTIVELLPVNGEFSL 540
QY 541 DDLQPHWSFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNIIKIEEISEVKMDAEF 600
Db 541 DDLQPHWSFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNIIKIEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFPAEDVGSNKGAIIGLMVGGVVIATVIFILVMLKKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFPAEDVGSNKGAIIGLMVGGVVIATVIFILVMLKKKQYTSIHGV 660
QY 661 VEYDAVTPERHLSKMOONGYENPTYKFFEQMONKK 697
Db 661 VEYDAVTPERHLSKMOONGYENPTYKFFEQMONKK 697

RESULT 11
US-09-794-743-16
: Sequence 16, Application US/09794743
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280BC
: CURRENT APPLICATION NUMBER: US/09/794,743
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-743-16

Query Match 99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNYQNGKWDSPSGTK 60
Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNYQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSECKVVEVAEEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSECKVVEVAEEVEE 240

QY 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRVPTTAASIPDAV 300
|||||
DB 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRVPTTAASIPDAV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
|||||
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQO:VETHMARVEAM:NDRR:ALENYIT:ALQAVPPRPRHVNMLK 420
|||||
DB 361 QEKVESLEQEAANERQO:VETHMARVEAM:NDRR:ALENYIT:ALQAVPPRPRHVNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLXVIYERMNOSLSLLYNVPAVA 480
|||||
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLXVIYERMNOSLSLLYNVPAVA 480
QY 481 BEIODEVDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
|||||
DB 481 BEIODEVDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
QY 541 DDLQPMHSEFGADSPANTENEVEPVDARPAADRGITTRPGSGLTNINIKIEISEVKMDAEF 600
|||||
DB 541 DDLQPMHSEFGADSPANTENEVEPVDARPAADRGITTRPGSGLTNINIKIEISEVKMDAEF 600
QY 601 RHDGSEYVHHQKLVFFAEADVGSNKGAIIGLMVGGVVATVIFITLVMKKKQYTSIHGV 660
|||||
DB 601 RHDGSEYVHHQKLVFFAEADVGSNKGAIIGLMVGGVVATVIFITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
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DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 12
US-09-794-748-16
: Sequence 16, Application US/09794748
: Patent No. US200200373:5A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280JL
: CURRENT APPLICATION NUMBER: US/09/794,748
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5, Re-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGALLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMNVQNGKWDSPSGTK 60
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DB 1 MLPGALLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKESILQYQCEVYPPELQITNNVEANQPVTONMCKRGKCKOCTHPHFVPIYRCLVG 120
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DB 61 TCIDTKESILQYQCEVYPPELQITNNVEANQPVTONMCKRGKCKOCTHPHFVPIYRCLVG 120
QY 121 EFVSALLVPKCKFLHQRMDVCETHLHWHVTAKETSEKSTNLHDYGMILLPGGIDKFR 180
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DB 121 EFVSALLVPKCKFLHQRMDVCETHLHWHVTAKETSEKSTNLHDYGMILLPGGIDKFR 180
QY 181 GVEFVCCPLAEESNVDSADAEEDDSOVWNGADTDYADGSEDKVVEVAEEVEEVEE 240
|||||
DB 181 GVEFVCCPLAEESNVDSADAEEDDSOVWNGADTDYADGSEDKVVEVAEEVEEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRVPTTAASIPDAV 300
|||||
DB 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRVPTTAASIPDAV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
|||||
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQO:VETHMARVEAM:NDRR:ALENYIT:ALQAVPPRPRHVNMLK 420
|||||
DB 361 QEKVESLEQEAANERQO:VETHMARVEAM:NDRR:ALENYIT:ALQAVPPRPRHVNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLXVIYERMNOSLSLLYNVPAVA 480
|||||
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLXVIYERMNOSLSLLYNVPAVA 480
QY 481 BEIODEVDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
|||||
DB 481 BEIODEVDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
QY 541 DDLQPMHSEFGADSPANTENEVEPVDARPAADRGITTRPGSGLTNINIKIEISEVKMDAEF 600
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DB 541 DDLQPMHSEFGADSPANTENEVEPVDARPAADRGITTRPGSGLTNINIKIEISEVKMDAEF 600
QY 601 RHDGSEYVHHQKLVFFAEADVGSNKGAIIGLMVGGVVATVIFITLVMKKKQYTSIHGV 660
|||||
DB 601 RHDGSEYVHHQKLVFFAEADVGSNKGAIIGLMVGGVVATVIFITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
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DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 13
US-09-794-925-16
: Sequence 16, Application US/09794925
: Patent No. US20020064819A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280HI
: CURRENT APPLICATION NUMBER: US/09/794,925
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-925-16

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-16

Query Match          99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPAQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPAQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GYEFVCCPLAESDNVDGADAEEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
Db 181 GYEFVCCPLAESDNVDGADAEEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 FADDEDEDDGDEVEEAEPEYEATERITSIATTTTTTTSVEEVVRVPTTAASPDVAV 300
Db 241 EADDEDEDDGDEVEEAEPEYEATERITSIATTTTTTTSVEEVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAFQKAKERLEAKHRMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQQLVETHMARVEAAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVTHLRYIYERMNOSLSLLYNVPAVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVTHLRYIYERMNOSLSLLYNVPAVA 480
QY 481 EEIQDEVDLLOKEQNYSDVLNMISEPRISYGNALMPSLTETKTVE-LPVGGEFSL 540
Db 481 EEIQDEVDLLOKEQNYSDVLNMISEPRISYGNALMPSLTETKTVE-LPVGGEFSL 540
QY 541 DDLOQWHSFGADSVPAANTENEVEPVDPADPAADRGLTTRPGSGLTNKTEEISEVKMDAEF 600
Db 541 DDLOQWHSFGADSVPAANTENEVEPVDPADPAADRGLTTRPGSGLTNKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEVDGSKNGKAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFAEVDGSKNGKAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 14
US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Helinikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; THEREOF
; FILE REFERENCE: 28341/6280FG
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; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-16
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Query Match          99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPAQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
Db 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPAQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GYEFVCCPLAESDNVDGADAEEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
Db 181 GYEFVCCPLAESDNVDGADAEEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 FADDEDEDDGDEVEEAEPEYEATERITSIATTTTTTTSVEEVVRVPTTAASPDVAV 300
Db 241 EADDEDEDDGDEVEEAEPEYEATERITSIATTTTTTTSVEEVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAFQKAKERLEAKHRMSOVMEWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQQLVETHMARVEAAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVTHLRYIYERMNOSLSLLYNVPAVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVTHLRYIYERMNOSLSLLYNVPAVA 480
QY 481 EEIQDEVDLLOKEQNYSDVLNMISEPRISYGNALMPSLTETKTVE-LPVGGEFSL 540
Db 481 EEIQDEVDLLOKEQNYSDVLNMISEPRISYGNALMPSLTETKTVE-LPVGGEFSL 540
QY 541 DDLOQWHSFGADSVPAANTENEVEPVDPADPAADRGLTTRPGSGLTNKTEEISEVKMDAEF 600
Db 541 DDLOQWHSFGADSVPAANTENEVEPVDPADPAADRGLTTRPGSGLTNKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEVDGSKNGKAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFAEVDGSKNGKAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
```

RESULT 15

US-09-869-414-16
: Sequence 16, Application US/09869414
: Publication No. US20030077226A1
: GENERAL INFORMATION:
: APPLICANT: Beinkowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE. APP SUBSTRATES THEREFOR, AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280M
: CURRENT APPLICATION NUMBER: US/09/869,414
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patent; Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-869-414-16

Query Match 99.8%; Score 3646; DB 11; Length 697;
Best Local Similarity 99.9%; P-Ed. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MLPGLALLLAANTARALEVPTDGNAGLLAEQIAMFCGRLLNNHNVQNGKWDSPSGTK	60
DB	1	MLPGLALLLAANTARALEVPTDGNAGLLAEQIAMFCGRLLNNHNVQNGKWDSPSGTK	60
QY	61	TCIDTREG:LOVCOEYYPELOITNVVEANQPTIQNKCKGRKQCKTHPHFVPIPYRCLVG	120
DB	61	TCIDTREGILOVCOEYYPELOITNVVEANQPTIQNKCKGRKQCKTHPHFVPIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLUQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKPR	180
DB	121	EFVSDALLVPDKCKFLUQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKPR	180
QY	181	GVFEVCCPLAEESDNDVSADAEEDSDVVMGADTDYADGSEDKVVEVAEEVEAEVEE	240
DB	181	GVFEVCCPLAEESDNDVSADAEEDSDVVMGADTDYADGSEDKVVEVAEEVEAEVEE	240
QY	241	EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTITTESVEEVVRYPTTAAS7PDAV	300
DB	241	EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTITTESVEEVVRYPTTAAS7PDAV	300
QY	301	DYLETIPGDENEHAHTQKAKERLEAKHRERMSQVMREKEEAEQAQKLPKADKAVIQHF	360
DB	301	DYLETIPGDENEHAHTQKAKERLEAKHRERMSQVMREKEEAEQAQKLPKADKAVIQHF	360
QY	361	QEKVESLEQPAANERQGLVETHMARVEAMLNDRRLALENYITALQAVPRPRHVFNMK	420
DB	361	QEKVESLEQPAANERQGLVETHMARVEAMLNDRRLALENYITALQAVPRPRHVFNMK	420
QY	421	KYVRAEQKDRQHTLKHFHVRMYDPKKAQIRSQVMTHLRVIIYERMNQSLSLLYNPAYA	480
DB	421	KYVRAEQKDRQHTLKHFHVRMYDPKKAQIRSQVMTHLRVIIYERMNQSLSLLYNPAYA	480
QY	481	RETODEVDELLQKSONYSDOVLANMISEPRISYGNALMPSLTETKTTHVL:PVNCFSL	540
DB	481	RETODEVDELLQKSONYSDOVLANMISEPRISYGNALMPSLTETKTTHVL:PVNCFSL	540
QY	541	DO:QPHWISFCADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNIKTBEISEVKMDAEP	600
DB	541	DO:QPHWISFCADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNIKTBEISEVKMDAEP	600

QY	601	RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGQVIATVIFITLVMKKKQXTSIHHGV	660
DB	601	RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGQVIATVIFITLVMKKKQXTSIHHGV	660
QY	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK	697
DB	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK	697

Search completed: October 2, 2003. 14:18:39
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:04 ; Search time 16.6667 Seconds
(without alignments)
4021.774 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
Sequence: 1 MLPGLALLLAANTARALEV.....QQNCYENPTIKFFPEQMKNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3636	99.5	695	A49795	Alzheimer's disease
2	3585.5	98.2	770	QHR0A4	Alzheimer's disease
3	3539	96.9	695	S00550	Alzheimer's disease
4	3514	95.2	595	A27485	Alzheimer's disease
5	3098	84.8	747	J60773	Alzheimer's disease
6	2105	57.6	484	A32761	hypothetical Alzhe
7	1723	47.2	763	A49321	amyloid beta (A β)
8	1711	46.8	765	S42880	amyloid precursor
9	1599	46.5	751	A49974	beta-amyloid precu
10	1180	32.3	653	A46362	amyloid precursor
11	1138	31.2	511	J61404	CDEI-box DNA-bindi
12	816.5	22.4	686	T15795	hypothetical prote
13	754	20.6	886	A32758	beta-amyloid-like
14	706	19.3	246	S38344	CDEI-binding prote
15	406	11.1	82	P00438	Alzheimer's disease
16	291.5	8.0	191	A35981	sperm membrane pro
17	278	7.6	57	E60045	Alzheimer's disease
18	278	7.6	57	E60045	Alzheimer's disease
19	278	7.6	57	G60045	Alzheimer's disease
20	278	7.6	57	D60045	Alzheimer's disease
21	278	7.6	57	A60045	Alzheimer's disease
22	278	7.6	57	B60045	Alzheimer's disease
23	217	5.9	42	PN0512	beta-amyloid prote
24	192.5	5.3	1110	2	NF-180 - sea lamp
25	185.5	5.1	407	1	immediate-early pr
26	184	5.0	5170	2	hypothetical prote
27	182	5.0	522	2	hypothetical prote
28	180.5	4.9	993	2	synaptonemal compl
29	179.5	4.9	1188	2	zinc finger protei

ALIGNMENTS

RESULT 1

A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (Crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisny, M.B.; Tolan, D.R.; Seikoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human support
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote.
C:Keywords: alternative splicing

Query Match	99.5%	Score	3636;	DB 1;	Length	695;			
Best Local Similarity	99.9%	Pred. No.	3.7e-184;						
Matches	694;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSDPSGK	60						
Db	1	MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSDPSGK	60						
Qy	61	TCIDTKESILQYCEVYPELQITNVVEANOPVTIQQNCKRGKCKTTPHFVFPYRCLVG	120						
Db	61	TCIDTKESILQYCEVYPELQITNVVEANOPVTIQQNCKRGKCKTTPHFVFPYRCLVG	120						
Qy	121	EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKFTCSKSTNLDHYGMLLPGCIDKFR	180						
Db	121	EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKFTCSKSTNLDHYGMLLPGCIDKFR	180						
Qy	181	GVEFVCCPLAESDNVSDADAEEDSDVWVGADTDVADGSEDKVVEAEVEEVAEVEE	240						
Db	181	GVEFVCCPLAESDNVSDADAEEDSDVWVGADTDVADGSEDKVVEAEVEEVAEVEE	240						
Qy	241	EADDEDEDEDEGDEVEEAEPEYEATERTTSIATITTTTTSVEEVVVPVPTTAASTPDV	300						
Db	241	EADDEDEDEDEGDEVEEAEPEYEATERTTSIATITTTTTSVEEVVVPVPTTAASTPDV	300						
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEAEAKNLPKADKAVIQHF	360						
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEAEAKNLPKADKAVIQHF	360						
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAIQAVPPRPRHVFNMLK	420						
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAIQAVPPRPRHVFNMLK	420						
Qy	421	KYVRAEQKDKQHTLKHFEHVRVMDPKKAAQIRSQVMTHLRVIYVERMNSLSLLYNVPAVA	480						

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810159
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St. George-Hyslop, P.; Van Kd
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dykes, I.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kanq, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pro
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1986
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <P02>
A:Cross-references: GB:X06989; EMBL:Y00287; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1986
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibiti
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
S:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Boer, F.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 506-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA

A:Residues: 507-770 <ZA>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for resid
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for res
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuth
Query Match 98.2%; Score 3585.5; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 1.9e-181;
Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;
Qy 1 MLPLGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNNHNMVQNGKWDSDSGTK 60
Db 1 MLPLGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNNHNMVQNGKWDSDSGTK 60
Qy 61 TCIDTKEGILQYCOEYVPELQITNVYEAQPVITQNMCKRGRKQCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELQITNVYEAQPVITQNMCKRGRKQCKTHPHFVPIYRCLVG 120
Qy 121 EFVSDALLYPDKCKFLHQRMDYCEIHLHWHYVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLYPDKCKFLHQRMDYCEIHLHWHYVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVVMWGGADTDYADGSEDKVVEVEAEVEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVVMWGGADTDYADGSEDKVVEVEAEVEEVEE 240
Qy 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTITTESVEEVVR----- 288
Db 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTITTESVEEVVR----- 288
Qy 289 ----- 288
Db 301 RAMLSRWYFDVTGSKCAPFYGGCGNRRNFOTEYCMVCGSAMSGSLKTIQEBLARD 360
Qy 289 ---VPTAASTPDVAVDKYLETPGDENEHAHFKAKERLEAKHRERMSQVMKEEAEERQA 345
Db 361 PVKLPTTAASTPDVAVDKYLETPGDENEHAHFKAKERLEAKHRERMSQVMKEEAEERQA 420
Qy 346 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAHLNDRRLALENYITAL 405
Db 421 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAHLNDRRLALENYITAL 480
Qy 406 OAVPPRPRHVFNMKKYVRAEQKDRQHTLKHFEHVRWMDPKAAQJRSQVMTHLRVIYER 465
Db 481 OAVPPRPRHVFNMKKYVRAEQKDRQHTLKHFEHVRWMDPKAAQJRSQVMTHLRVIYER 540
Qy 466 MNGSLSLIYNVPVAPAEIODEVDDELLOKEONYSDVLANMISEPRIISYGNDAIMPSTET 525
Db 541 MNGSLSLIYNVPVAPAEIODEVDDELLOKEONYSDVLANMISEPRIISYGNDAIMPSTET 600
Qy 526 KTIIVELLPVNGEFTSLDLPQWHSFGADSVPAANTENEVEPYDADPAADRGLTTTPSGSLTN 585
Db 601 KTIIVELLPVNGEFTSLDLPQWHSFGADSVPAANTENEVEPYDADPAADRGLTTTPSGSLTN 660
Qy 586 IKTEEISEVKMDAEFRHDSGYEVHHOKLVHFAEDVGSNGKGAIIGLVMGVVATVITIL 645
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVHFAEDVGSNGKGAIIGLVMGVVATVITIL 720
Qy 646 VMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695
Db 721 VMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, G.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg,
EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:8832583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:q55616; PIDN:CAA30488.1; P.D:q55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 233-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2468652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behar, D.; Masters, C.L.; Multhaup, G.
FEBS Lett 345, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein: binding to copper.
A:Reference number: S45251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1673481
A:Accession: A39820
A:Molecule type: protein
A:Status: preliminary
A:Residues: 18-32 <PO>
A:Experimental source: brain
A:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane *status predicted <TM>
Query Match 96.9%; Score 3539; DB 2; Length 695;
Best Local Similarity 97.1%; Pred. No. 4.8e-179;
Matches 675; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVTPYRCLVG 120
DB 61 TCIGTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
DB 181 GVEFVCCPLAESDIDSADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
QY 241 EADDEDEDEGDEVEAEPEEATERTTSIAITTTTITESTESVEEVVPTTAASPTDAV 300
DB 241 EADDEDEDEGDEVEAEPEEATERTTSIAITTTTITESTESVEEVVPTTAASPTDAV 300
QY 301 DKYLETPGDENEHAHFOKAKERI, EAKHRRMSQVMREWEAEARQAKNPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEARQAKNPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQOOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVENMLK 420
DB 361 QEKVESLEQEAANERQOOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVENMLK 420
QY 421 KYVRAEQKQRHTLKHFEHVRVMDPKAAQIRSQVMTHLRVIVYERNQSLSLLYNYPAVA 480
DB 421 KYVRAEQKQRHTLKHFEHVRVMDPKAAQIRSQVMTHLRVIVYERNQSLSLLYNYPAVA 480
QY 481 EETQDEVELLOKEQNSDDVLNMISEPRISYGNALMPSLTETKTITVELLPVNGEESL 540
DB 481 EETQDEVELLOKEQNSDDVLNMISEPRISYGNALMPSLTETKTITVELLPVNGEESL 540

QY 541 DDLQPHWSPGADSVSPANTENEVPEVDARPAADRGLLITRPGSLTNIKTEETSEVKMDAEF 600
DB 541 DDLQPHWSPGADSVSPANTENEVPEVDARPAADRGLLITRPGSLTNIKTEETSEVKMDAEF 600
QY 601 RHDSEYEVHOKLVFFAEDVGSNKCAITGLMVGVIATVITLVMKKKQYTSIHGV 660
DB 601 GHDSFEVHOKLVFFAEDVGSNKCAITGLMVGVIATVITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPFERHLSKMOONGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPFERHLSKMOONGYENPTYKFFEQMON 695
RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alzheimer names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Iamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein
A:Reference number: A27485; MUID:88106489; PMID:332280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085
A:Experimental source: brain
R:De Strooper, B.; van Leuven, F.; van Bergh, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Izumii, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzhe
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:q220328; PIDN:BA001456.1; PID:q220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C:Keywords: alternative splicing; amyloid; transmembrane protein
Query Match 96.2%; Score 3514; DB 2; Length 695;
Best Local Similarity 96.7%; Pred. No. 9.9e-178;
Matches 672; Conservative 5; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVTPYRCLVG 120
DB 61 TCIGTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
DB 181 GVEFVCCPLAESDIDSADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
QY 241 EADDEDEDEGDEVEAEPEEATERTTSIAITTTTITESTESVEEVVPTTAASPTDAV 300

```
Db 241 EADDSEVDEGDEVEEAEPEYERATERT:STATTTTTTSTESVEEVVVFVTTTAASTPDV 303
Qy 301 DKYLETPGDENEHAHFQKAKERLEAKIRHRMSQVMREWEAEQAQKNI:PKADKKAVIQRP 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKIRHRMSQVMREWEAEQAQKNI:PKADKKAVIQRP 360
Qy 361 QEKVESLEQAANEERQQLVETHMARVEAMLNDRRLALENYITAIQAVPPRP:RVFNMLK 420
Db 361 QEKVESLEQAANEERQQLVETHMARVEAMLNDRRLALENYITAIQAVPPRP:RVFNMLK 420
Qy 421 KYVRAEQKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNQSLSLYNPAVA 480
Db 421 KYVRAEQKDRQHTLKHFHVRVMDPKKATQIRSOVMTHLRVYERMNQSLSLYNPAVA 480
Qy 481 BEIODEVELLQKEQNTSDOVLANMISEPRISYGNDAIMPSTLTETKTIVVLLPVGNGEFSL 540
Db 481 BEIODEVELLQKEQNTSDOVLANMISEPRISYGNDAIMPSTLTETKTIVVLLPVGNGEFSL 540
Qy 541 DDLOPHSFGADSVPAANTEVEVPDARPAADRGTLTRPGSLTNIKTEELISEVKMDAEP 600
Db 541 DDLOPHSFGADSVPAANTEVEVPDARPAADRGTLTRPGSLTNIKTEELISEVKMDAEP 600
Qy 601 RHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGWGIATVITFLVLMKKKQYTSIHGV 660
Db 601 GHDSGFVRRHQLVFAEDVGSNKGAIIGLMVGWGIATVITFLVLMKKKQYTSIHGV 660
Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 *sequence_revision 10-Jun-1993 *text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homolog of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1262805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:q263150; PIDN:AB24853.1; PID:q263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein: animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 84.8%; Score 3098; DB 2; Length 747;
Best Local Similarity 80.9%; Pred. No. 6.7e-156;
Matches 597; Conservative 35; Mismatches 42; Indels 64; Gaps 5;

Qy 17 ALEYPTDGNAGLLAEPQIAMP-CGRLLNHNHNVQNGKSDSPSGTKCIDTKESILQYQCE 75
Db 15 ALEVLDGNSGGLLAEPQ:AMF:SVARLNNHNNVQNGKMETVSG---CIGTKESG:LYQYQCE 71
Qy 76 VYPELQITNVVEANQPVYTIQNWCKRGKQCKTHPHFVIPYRCVLGGEVFSQALLVPDKCKF 135
Db 72 VYPELQITNVVEANQPVYTIQNWCKRGKQCKTHPHFVIPYRCVLGGEVFSQALLVPDKCKF 131
Qy 136 LHQERMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKPRGVEFFVCCPLAESDN 195
Db 132 LHQERMDICETHLHHHTVAKESKSKSLHEYGMLLPCGIDKPRGVEFFVCCPLAESSES 191
Qy 196 VDSADAECDQVMWGGADTDYADGSEDKVVEVA--EEEEVAEEVEEADDEDDDEDCDE 253
Db 192 FDSADAECDQVMWGGADTDYVDRSDKAVEAQPDDEEEVVEVEEETDDEDD--DGDE 249
Qy 254 VEEAEPEYERATERT:SIATTTTTTSTESVEEVVVFVTTTAASTPDV 303
Db 254 VEEAEPEYERATERT:SIATTTTTTSTESVEEVVVFVTTTAASTPDV 303
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Db 250 AESEPEPEYERATERT:SIATTTTTTSTESVEEVVVFVTCSEQAETGPCRAMISRMYDYVTE 309
Qy 289 -----VPTTAASTPDVADVKILETPGDENEHAHFQ 317
Db 310 SKCAQFIYGGCGGNRRNFESDDYCHAVCGSVIPATAASTPDVADVKYLENPNDENEHDFEL 369
Qy 318 KAKERLEPAKIRHRMSQVMREWEAEQAQKNI:PKADKKAVIQHFOEKVES:EQEAANEERQ 377
Db 370 KAKERLEGGKHKREKMSVKMEWEAEQAQKNI:PKADKKAVIQHFOEKVES:EQEAANEERQ 429
Qy 378 LVETHMARVEAMLNDRRLALENYITAIQAVPPRP:RVFNMLK:KKYVRAEQKDRQHTLKHF 437
Db 430 LVETHMARVEAMLNDRRLALENYITAIQADPPRP:RVFNMLK:KKYVRAEQKDRQHTLKHF 489
Qy 438 EHVRYMDPKKAAQIRSOVMTHLRVYERMNQSLSLYNPAVAEEIODEVELLQKEQNT 497
Db 490 EHVRYMDPKKAAQIRSOVMTHLRVYERMNQSFSLYKVPVAEEIODEVELLQKEQNT 549
Qy 498 SDOVLNMISEPRISYGNDAIMPSTLTETKTIVVLLPVGNGEFSUDDLQPHSFGADSVPA 557
Db 550 SDOVMNMYSDHRVSYGNDAIMPSTLTETKTIVVLLPVDGEFNIEDLQPHSFGVDSVPA 609
Qy 558 TENEVFPDARPAADRGTLTRPGSLTNIKTEELISEVKMDAERHDSGYEVHHQKLVFPA 617
Db 610 TENEVFPDARPAADRGTLTRPGSLTNIKTEELISEVKMDSEYRHDATAYEVHHQKLVFPA 669
Qy 618 EDVGSNKGAIIGLMVGWGIATVITFLVLMKKKQYTSIHGVVEVDAAVTPEERHLSK 677
Db 670 EYVGSNKGAIIGLMVGWGIATVITFLVLMKKKQYTSIHGVVEVDAAVTPEERHLSK 729
Qy 678 QONGYENPTYKFFEQMON 695
Db 730 QONGYENPTYKFFEQMON 747

RESULT 6
A32761
hypoetical Alzheimer's disease amyloid beta protein, Alu-containing clone - huma
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 *sequence_revision 10-Apr-1996 *text_change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secre
A:Reference number: A32761; MUID:89346754; PMID:2569763
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DFS>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as leu
C:Comment: This is the hypothetical translation of a sequence believed to contain
C:Keywords: cloning artifact

Query Match 57.6%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 9.9e-104;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;

Qy 80 LQITNVVEANQPVYTIQNWCKRGKQCKTHPHFVIPYRCVLGGEVFSQALLVPDKCKF 139
Db 1 LQITNVVEANQPVYTIQNWCKRGKQCKTHPHFVIPYRCVLGGEVFSQALLVPDKCKF 60
Qy 140 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKPRGVEFFVCCPLAESDNVDSA 199
Db 61 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKPRGVEFFVCCPLAESDNVDSA 120
Qy 200 DAEEDSDQVMWGGADTDYADGSEDKVVEVAEEVEEVEEADDEDDDEDDGDEVEEEAE 259
Db 121 DAEEDSDQVMWGGADTDYADGSEDKVVEVAEEVEEVEEADDEDDDEDDGDEVEEEAE 180
Qy 260 EPEYERATERT:SIATTTTTTSTESVEEVVVFVTTTAASTPDV 303
Db 181 EPEYERATERT:SIATTTTTTSTESVEEVVVFVTCSEQAETGPCRAMISRMYDFVTEGKCAPF 240
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QY 289 -----VPTTAASTPDADVKYLETPTGDNENHAFQAKERL 323
Db 241 FYGCGGGRNNFTDEEYCMVCGSAPTTAASTPDADVKYLETPTGDNENHAFQAKERL 300
QY 324 EAKHRRMSQVMEWEAEARQAKNPKADKAVIQHFQKVESLEGEAEANERQQLVFETHM 363
Db 301 EAKHRRMSQVMEWEAEARQAKNPKADKAVIQHFQKVESLEGEAEANERQQLVFETHM 360
QY 384 ARVEMMLNDRRLALENYITALQAVPRPRHVNFMILKKYVRAEQKDRQHILKHFSDIVRVV 443
Db 361 ARVEMMLNDRRLALENYITALQAVPRPRHVNFMILKKYVRAEQKDRQHILKHFSDIVRVV 420
QY 444 DPKKAAQIRSQVTHLRYTYERNQSLSLLYNYPVAVAEIODEV 487
Db 421 DPKKAAQIRSQVTHLRYTYERNQSLSLLYNYPVAVAEIODEV 464

RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
N:Alternate names: CDE1-binding protein
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence.revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A49321; S34644; S40519
R:Spencer, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A:Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: c
A:Reference number: A49321; MUID:93250009; PMID:8485127
A:Accession: A49321
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
A:Cross-references: GB:S60099; NID:g300168; PIDN:AAC60583.1; PID:g300169
A:Experimental source: placenta
A:Note: Sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P:131195)
R:von der Kammer, H.; Klaidiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL data library, April 1993
A:Description: The human homologue of the murine CDE1 binding protein is an amyloid pre
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <VON>
A:Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA60295.1; PID:g394764
R:Masco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A:Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94035131; PMID:8220435
A:Accession: S40519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C:Genetics:
A:Gene: GDB:APLP2; APLP2
A:Cross-references: GDB:l139159; OMIM:l04776
A:Map position: 11q23-11q25
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <RPI>

Query Match 47.2% Score 1723; DB 2; Length 763;
Best Local Similarity 47.0% Pred. No. 2.3e-83;
Matches 371; Conservative 112; Mismatches 166; Indels 140; Gaps 20;
QY 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEFQIAFMFCGRLLNMHNVQNGKDSPP 56
Db 15 LELLLLGGTAPALAGLYEALAAAGTGFVAEPEQIAMFCGKLMHVNITQIGKWEPP 7;
QY 57 SGRTGIDTKEGILQCOEYVPELQITNVVEANOPTVQNCWCKRGKCKTTPHFVYPR 116
Db 75 TGTKSCFETKEEVLYQCOEWPELQITNVVEANORVSDNWCRRDKKQCKS--RFTWPK 132

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RESULT 8

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S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence.revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid p;
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

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C:Keywords: alternative splicing

F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.8%; Score 1711; DB 2; Length 765;
Best Local Similarity 46.1%; Pred. No. 9, 8e-23;
Matches 363; Conservative 122; Mismatches 157; Indels 136; Gaps 20;

QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPOIAMFCGRIMHNNVNGKWDSP 56
DB 15 LVLVLLGLTAPAAALAGYIEALANAGTGFVAEPQIAMFCGKLNHVNIGTKWEPP 74
QY 57 SGTKCIDTKEGILQYCCQEVPELOITNVVEANQPTIONMCKRGKCKTKPHFVIPYR 116
DB 75 TGTKSLGTKEEVLYQYCCQEIYPELOITNVVEANQPTIONMCKRGKCKTKPHFVIPYR 132
QY 117 CLVGFVSVDALLVPDKCKFLHQRMDVCEYTHLHMHIVAKETCEKSTNLHDYGMLLPGCI 176
DB 133 CLVGFVSVDLLVPDNCQPFHQERMEVCEKHQRWHTLVKAECLTEGLTLYSYGMLLPGCV 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYA--DGSEDKVVEVAFEE 233
DB 193 DQFHGTGYCCPOTKYVDSSTMSKEEEEE-----DEEDYALGKSEFPTEAGLEDT 248
QY 234 VAEEVEEADDDDDGDEVEEAEPEYEE-----ATERTISATTTITTESVEFVY 287
DB 249 EAAADEDEDEEEEGEEVVEDROYDYDFKGDYNEENPTPESSDGTISIKELAHDV 308
QY 288 R-----VPT 291
DB 309 KAVCSOEAMTGPCRAVPRWYFDSLKGKCVRFYIGCGGNRNFSEDCYMAVCKTMIP 368
QY 292 TAASTPDVDKYLETPGDENEHAFKAKERLEAKHRRMSQVWRWEFAERCAKNLPKA 353
DB 369 TPLPTND--VDVYFETSAADNEHARFQAKERLEIRHRRMDRVKKEWEAEALGAKNLPKA 427
QY 352 DKKAVTQHFQKESLQFAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPR 411
DB 428 ERQTLIQHFQAMVKALEKAASEKQQLVETHLARVEAMLNDRRLALENYLAALQSDPPR 487
QY 412 PRHVNMLKYYRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVTHLRYIYERMGSL 471
DB 488 PHRIQLARVYRAENKRLHTIRHYQHLAVDPEKAAQKQVMTHLRVIEERNGSL 547
QY 472 LLVNPVAAVEIODEVELLQKQNYSDVLANKISEPRISYGNDAIMPSTLTKTIVEL 531
DB 548 ELKVPYVAQIEDEIDELQEQR-----ADM-----DQTSISENPVDVR-- 589
QY 532 LPVNGEFLDLOPWHFSFGADSPANTENEVEPVDARPAADRLTTPGSGSLN----- 586
DB 590 --VSSEES-EEIPPHLPF--RPFSLSENE-----DQPELYHPM--KKGSNAFQDQGL 638
QY 587 KTEE---ISEVKMDAEFRHDSGYEVHHQKLVFAEDVGS-----NKG 626
DB 639 GAEEKVINSKNMKNMNNVIDETLDV--KEMIFNAERYGGLLEEPDSVGPLKEDFSLSSA 696
QY 627 IIGLMVGGVVIATVIFITLVMLKKQVYISHHGVEVDAAVTPEERHLSKMOONGYENPT 686
DB 697 LIGLVVIAVAIATVIVISLVMLKRRQGTISHGIVEVDPMLTPEERHLNKNQNHGIE 756
QY 687 YKFEQMQ 694
DB 757 YKYLEQMQ 764

RESULT 9

A49974

beta-amyloid precursor protein 2 homolog APLP2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1993

C:Accession: A49974

R:Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.

J. Biol. Chem. 269, 2637-2644, 1994

A:Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid

A:Reference number: A49974; MUID:94132029; PMID:8300594

A:Accession: A49974

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-751 <SLD>

A:Cross-references: GB:U1557; NID:q558467; PIDN:AAA50603.1; P-D:q558468

A:Note: sequence extracted from NCBI backbone (NCBIP:144636)

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei

F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.5%; Score 1699; DB 2; Length 751;

Best Local Similarity 45.8%; Pred. No. 4, 1e-82;

Matches 362; Conservative 113; Mismatches 160; Indels 156; Gaps 20;

QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPOIAMFCGRIMHNNVNGKWDSP 56
DB 15 LVLVLLGLTAPAAALAGYIEALANAGTGFVAEPQIAMFCGKLNHVNIGTKWEPP 74
QY 57 SGTKCIDTKEGILQYCCQEVPELOITNVVEANQPTIONMCKRGKCKTKPHFVIPYR 116
DB 75 TGTKSLGTKEEVLYQYCCQEIYPELOITNVVEANQPTIONMCKRGKCKTKPHFVIPYR 132
QY 117 CLVGFVSVDALLVPDKCKFLHQRMDVCEYTHLHMHIVAKETCEKSTNLHDYGMLLPGCI 176
DB 133 CLVGFVSVDLLVPDNCQPFHQERMEVCEKHQRWHTLVKAECLTEGLTLYSYGMLLPGCV 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYA--DGSEDKVVEVAFEE 231
DB 193 DQFHGTGYCCPOTKYVDSSTMSKEEEEE-----DEDEEEDYDJKSEFPTE 243
QY 232 EEAEEVEEAD--DDEDDGDEVEE-----AEEPYEATERTTISIATT 276
DB 244 ADLEDFTEAADADEEEDDEEVEVVEDROYDYDFKGDYNEENPTPESSGTIS----- 298
QY 277 TTTTSEVEE----- 286
DB 299 --DKEIVHDKAVCSOEAMTGPCRAVPRWYFDSLKGKCVRFYIGCGGNRNFSEDCY 356
QY 287 -----VRVPTTAASTPDVDKYLETPGDENEHAFKAKERLEAKHRRMSQVWRWEFA 341
DB 357 MAVCKAMIPPTPLPTND--VDVYFETSAADNEHARFQAKERLEIRHRRMDRVKKEWEA 415
QY 342 ERQAKNLPKADKAVTQHFQKESLQFAANERQQLVETHMARVEAMLNDRRLALENY 401
DB 416 ELOAKNLPKTEROTLIQHFQAMVKALEKAASEKQQLVETHLARVEAMLNDRRLALENY 475
QY 402 ITALQAVPPRPHRVFNMKKYYRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVTHLRY 461
DB 476 LAALQSDPPRPHRIQLARVYRAENKRLHTIRHYQHLAVDPEKAAQKQVMTHLRV 535
QY 462 IYERMGSLLLVNPVAAVEIODEVELLQKQNYSDVLANKISEPRISYGNDAIMP 521
DB 536 IEERRNOSLLYKVPYVAQIEDEIDELQEQR-----ADM-----DQTS 578
QY 522 LITKTKTVELLPPVNGEFLDLOPWHFSFGADSPANTENEVEPVDARPAADRLTTPGSG 581
DB 579 ISENPDVVRVSSSE-EEIPPHLPF-----PULSENE-----GSCMAEQDG- 621
QY 582 GLTNIKTEEL-SEVKMDAEFRHDSGYEVHHQKLVFAEDVGS-----N 623
DB 622 GLTGAEEKVINSKNMKNMNNVIDETLDV--KEMIFNAERYGGLLEEPDSVGPLKEDFSL 679
QY 624 KGALIGLMVGGVVIATVIFITLVMLKKQVYISHHGVEVDAAVTPEERHLSKMOONGYE 683
DB 680 SNALIGLVVIAVAIATVIVISLVMLKRRQGTISHGIVEVDPMLTPEERHLNKNQNHGIE 739
QY 684 NPTYKFEQMQ 694
DB 740 NPTYKYLEQMQ 750

RESULT 10

A46362

amyloid precursor-like protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:WASCO, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
 proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer's disease amyloid precursor protein.
 A:Reference number: A46362; MIM:93086322; PMID:1279893
 A:Accession: A46362
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:118683, NCBI:118584)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal knittz-type proteinase
 C:Keywords: transmembrane protein

[illegible]

RESULT 11
JC1404

CDEI-box DNA-binding protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
 C:Accession: JC1404
 R:Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
 Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
 A:Title: A murine sequence-specific DNA binding protein shows extensive local simi
 A:Reference number: JC1404; MUID:93129193; PMID:1482349
 A:Accession: JC1404
 A:Molecule type: mRNA
 A:Residues: 1-511 <VID>
 C:Comment: This protein plays an important role in the early development of the mo
 C:Keywords: DNA binding; transmembrane protein

```

Query Match      31.2%: Score 1138; DB 2: Length 511;
Best Local Similarity 45.6%: Pred. No. 8.8e-53;
Matches 252: Conservative 92; Mismatches 129; Indels 80; Gaps 16;

174 CGIDKRGVEFVGCPIAE--ESDNVDSALAEEDSDVMWGGADTDYAXGSEDKVWEAE- 230
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6 CGVDQFHGTGYVCCPOTKVTDSDDSTMSKEEBEE-----DDEDEEDYDLKSEF 56

231 --EEEAEEVEEAD--DDEDDGDGEVEAE-----EPYEAERTSTIAITTTT 279
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
57 PEAHJEDFTEAAADFEEDDEEAGEEVEDRYDYPFKGDYNE--ENPTFSSGCTIS 114

280 TESVEEVVRPTTAASTPOAVDKYLETGPDENSHAHFQKAKERLEAKHRMSQVMRE 339
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
115 DKEIVHDVKKVPPTPLTND--VDVYFETADDNHAFQKAKEOLEIHRNRMDRVKWE 173

340 EAEKQAKNI PKAUKAVIOHFQEKVKSLEQEAANEHQQLVETHMAKVEAMLNDRRLALE 359
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
174 EAELOAKNLPKTERQTLIOHFQAMVKALEKAAASEKQQLVETHLARVAMLNDRRIALE 233

400 NYTTALQAVPPRZHRVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKAAQITSQWTHL 459
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
234 NYTAAEQSDPPRHRILQALRRYVRAENKDLHTIRHYQVLAVDPDEKAAQMSQWYTHL 253

460 RVTYERMSQSLLYNYPVAAEEIOEDVELQKEONYSDDVLANNITSEPPRISYGNDA 519
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
294 HVTEERNQSLLYKVPVAAQIEIEIDELQEQR-----ADM-----DQFT 336

520 PSUTERTKTIVELLPVNGEHSLODLQVHSGAGSDSPANTENEVEPVDARPAADRGUTTRP 579
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
337 SSISEPNVDVRVSSSESE-EIPPFHLHPF-----FSLSENE-----GSGMAEQD 380

580 GSGLTNIKITEEI-SEYKMDAEFRHDSGYEVHHQKLVFEAEVDGS----- 622
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
381 G-GLJCAEEKVINSKNKMDENMYIDETLDV--KEMIFNAERVGGLDEEPESVGPLREDFS 437

623 -NKGATIGLVGAGVATVYIFITLVMLKKQYTSIHHGVYEVDAATPBERRHLSKMOONG 681
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
438 LSSNALIGLLVIAVATVIVISVLWRKNQVGTISHGIVEVDPMLTPEERHLKNNQNHG 497

682 YENPTYKPFQEQM 694
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
498 YENPTYKYLEQM 510
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 12
"15795"

hypothetical protein C42D8.8 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
 C:Accession: F15795; A49414
 R:Hallsworth, K.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of *C. elegans* cosmid C42D8.
 A:Reference number: Z18405
 A:Accession: F15795
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-686 <HAL>

QY 520 -----PSLTETKTYVELLPVNGEFLSDLDLQPMHSEFGADSVFANTENEVEPVDARPAADRG 574
DB 714 VTAANPNLETTKS-----EKDLSDE-----YGEATVSTKVTLPVDDAVQORA 760
QY 575 LTRPGSGLTNIKITEISEVKMDAEFRHDSGYEVHHQKLVF-----FAEDVGSNK---GA 626
DB 761 VEDVANA-----VAHOEAEPQVOHMTEDLGHRESSFSRLREFAQHAAHAKGRNV 811
QY 627 IGLKVGGVVIAVIFITLVNCKKQYYSIH-HGVVEVDAAVTP-----FERHLSKXQO 679
DB 812 YFTFSFAGTALMAAVFVGAVAKWRISPSRAGGFIENDQNVITHPTVREKIVPNMOI 871
QY 680 NGYENPTYKFFE 691
DB 872 NGYENPTYKFE 883

RESULT 14

S38344

CDEI-binding protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1995

C:Accession: S38344

R:Hanes, C.; von der Kammer, H.; Kristjansson, G.; Scheit, K.H.

Biochim. Biophys. Acta 1216, 154-156, 1993

A:Title: The complete cDNA coding sequence for the mouse CDEI binding protein.

A:Reference number: S38344; MUID:94032480; PMID:8218408

A:Accession: S38344

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-246 <HAN>

A:Cross-references: EMBL:222592

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 19.3%; Score 706; DB 2; Length 246;
Best Local Similarity 51.5%; Pred. No. 2e-30;
Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;

QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPOIAMFGRLNMHMNVONGKWDSP 56
DB 15 LVLVLLGLUTAPAAALAGVIEALAAAGTGFVAEPOIAMLCGLNMHVNIOIGKWEDEP 74
QY 57 SGTKICIDTKEGLOYCQYVPELOITNVVEANQPTVIONMCKRGKCKKTHPHFVPIYR 116
DB 75 TGIKSLGTKEEVLOYCQYVPELOITNVVEANQPTVIONMCKRGKCKKTHPHFVPIYR 132
QY 117 CLVGEFVSQALLVPCKCKLHQRMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGI 176
DB 133 CLVGEFVSQALLVPCKCKLHQRMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGI 192
QY 177 DKFRGVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSHDKYVEVAEEVAF 236
DB 193 DQPHGTEYVCCP---QTKIVDS-----DSIMSKEEKEE--- 222
QY 237 VEEEDADDED-DEGDVEVEEAE 259
DB 223 -EEDEDEDEEDYDLKSEFPTEAD 245

RESULT 15

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroux, L.F.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A:Reference number: PQ0438; MUID:93075180; PMID:1445331

A:Accession: PQ0438

A:Molecule type: DNA

A:Residues: 1-82 <DAV>

A:Cross-references: GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 11.1%; Score 406; DB 2; Length 62;
Best Local Similarity 98.8%; Pred. No. 3.1e-15;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 581 SGLTNIKTEELSEVKMDAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIGLMVGGVVATV 640
DB 1 SGLTNIKTEELSEVKMDAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIGLMVGGVVATV 63
QY 641 IFITLVMLKKKKQYTSIHGGVVE 662
DB 61 IVITLVMLKKKKQYTSIHGGVVE 82

Search completed: October 2, 2003, 14:00:36

Cdb time : 19.5667 secs

GenCore version: 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 10 seconds
(without alignments)
3277.761 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
Sequence: 1 MLPGLALLLAANTARALEV.....QOQYENPTYKFFEQMONKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358.5	98.2	770	1 A4_HUMAN	P05067 h amyloid b
2	358.5	98.2	770	1 A4_MACFA	P53601 m amyloid b
3	357.9	98.0	751	1 A4_SAISC	G95241 s amyloid b
4	353.0	96.6	770	1 A4_PIG	P79307 s amyloid b
5	351.7	96.3	770	1 A4_CAVPO	G62495 c amyloid b
6	348.5	95.5	770	1 A4_MOUSE	P12023 m amyloid b
7	348.5	95.5	770	1 A4_RAT	P03592 r amyloid b
8	1730	47.4	695	1 APP2_MOUSE	Q06335 mus musculu
9	1723	47.2	763	1 APP2_HUMAN	Q06481 homo sapien
10	1711	46.8	765	1 APP2_RAT	P15943 rattus norv
11	1185	32.4	650	1 APP1_HUMAN	P51693 homo sapien
12	1180	32.3	653	1 APP1_MOUSE	Q03157 mus musculu
13	816.5	22.4	686	1 A4_CAEEL	Q10651 caenorhabdi
14	755.5	20.7	887	1 A4_DROME	P14599 drosophila
15	287	7.9	58	1 A4_BOVIN	Q28053 bos taurus
16	283	7.7	58	1 A4_RABIT	Q28748 oryctolagus
17	283	7.7	58	1 A4_SHEEP	Q28757 ovis aries
18	282	7.7	58	1 A4_CANFA	Q28280 canis famil
19	278	7.6	57	1 A4_URSMA	Q29149 ursus marit
20	185.5	5.1	407	1 IE68_HSV5A	Q01042 herpesvirus
21	180.5	4.9	993	1 SCPI1_MOUSE	Q62209 mus musculu
22	176	4.8	2004	1 M02_HUMAN	Q29794 homo sapien
23	175.5	4.8	802	1 NAB3_YEAST	P38996 saccharomyc
24	174	4.8	579	1 G160_HUMAN	Q08378 homo sapien
25	173.5	4.7	793	1 CALD_HUMAN	Q05682 homo sapien
26	172	4.7	771	1 CALD_CHICK	P12957 gallus gall
27	169.5	4.6	297	1 TRT2_HUMAN	P45379 homo sapien
28	169.5	4.6	721	1 YCF2_OENPI	P15568 oenothera p
29	168.5	4.6	1875	1 MLPI1_YEAST	Q02455 saccharomyc
30	168	4.6	1240	1 YNJ1_YEAST	P35935 saccharomyc
31	167.5	4.6	1976	1 MYHA_HUMAN	P35580 homo sapien
32	166.5	4.6	816	1 YG3A_YEAST	P53278 saccharomyc
33	166.5	4.6	1976	1 MYHA_RAT	Q931t0 rattus norv

34	164.5	4.5	1325	1 G160_MOUSE	P55937 mus musculu
35	163.5	4.5	681	1 MP10_HUMAN	Q00566 homo sapien
36	162.5	4.4	712	1 NUCCL_RAT	P13383 rattus norv
37	162	4.4	2017	1 MYSN_DROME	Q99323 drosophila
38	160.5	4.4	1976	1 MYHA_BOVIN	Q27991 bos taurus
39	160	4.4	694	1 NUCCL_CHICK	P15771 gallus gall
40	159.5	4.4	1955	1 PUMA_PARUN	O61308 parascaris
41	158	4.3	301	1 TRT2_CHICK	P02642 gallus gall
42	157.5	4.3	706	1 NUCCL_HUMAN	P19348 homo sapien
43	156.5	4.3	5596	1 MDNI_HUMAN	Q9nu22 homo sapien
44	156	4.3	1332	1 SPI7_YEAST	P35177 saccharomyc
45	156	4.3	1433	1 REST_CHICK	O42184 gallus gall

ALIGNMENTS

RESULT 1					
A4_HUMAN					
ID	A4_HUMAN	STANDARD:	PRT:	770 AA.	
AC	P05067	P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q9BT38;			
AC	Q9UCB6; Q9UQ58;				
DT	13-AUG-1987	(Rel. 05, Created)			
DT	01-NOV-1991	(Rel. 20, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CRF(59) (Gamma-secretase C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57) (Amyloid intracellular domain 57) (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain 50) (AID(50)); C31].				
GN	APP OR A4 OR ADL				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
FN	[1]	SEQUENCE FROM N.A. (ISOFORM APP695).			
RP	I-TSSUP=BtaIn;				
RC	I-TSSUP=BtaIn;				
KX	MEDLINE=87144572; PubMed=2881207;				
RA	Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;				
RA	"The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.";				
RI	Nature 325:733-736(1987).				
RL	[2]	SEQUENCE FROM N.A. (ISOFORM APP751).			
RP	I-TSSUP=BtaIn;				
KC	MEDLINE=H8122635; PubMed=2894289;				
RA	Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;				
RA	"A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors.";				
RT	Nature 331:525-527(1988).				
RL	[3]	SEQUENCE FROM N.A. (ISOFORM APP695).			
RP	MEDLINE=89128427; PubMed=2783775;				
RX	Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;				
RA	"The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.";				
RL	Nucleic Acids Res. 17:517-522(1989).				
RN	[4]	SEQUENCE FROM N.A. (ISOFORM APP770).			
RP	MEDLINE=90236318; PubMed=2110105;				
RX	Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;				
RA	"Genomic organization of the human amyloid beta-protein precursor gene.";				
RT					

RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 secreted protein";
 RA Science 245:651-653(1989).
 RL [14]
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORM APP733).
 RP TISSUE=Leukocyte; PubMed:1587857;
 RA MEDLINE-92288116; PubMed:1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells";
 RA J Biol. Chem. 267:10804-10809(1992).
 RL [7]
 RN SEQUENCE FROM N.A. (ISOFORM APP770).
 RP MEDLINE-97263807; PubMed:9108164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus";
 RA Nucleic Acids Res. 25:1802-1808(1997).
 RL [8]
 RN SEQUENCE FROM N.A. (ISOFORM APP305).
 RP TISSUE=Pancreas;
 RA MEDLINE-22388257; PubMed:2477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derue J.G.,
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang G., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loquellaro N.A., Peters G.J., Abramson R.D., Millady S.C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vialation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [9]
 RN SEQUENCE OF 1-10 FROM N.A.
 RP TISSUE=Liver;
 RA MEDLINE-89016647; PubMed:3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide";
 RA Nucleic Acids Res. 15:9351-9351(1988).
 RL [10]
 RN ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RL [11]
 RN SEQUENCE OF 1-75 FROM N.A.
 RA MEDLINE-89165870; PubMed:2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene";
 RA Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RL [12]
 RN SEQUENCE OF 18-50.
 RP TISSUE=Fibroblast;
 RA MEDLINE-87250462; PubMed:3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts";
 RA J. Biol. Chem. 262:8508-8514(1987).

RN [13]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE-89346754; PubMed:2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 secreted protein";
 RA Science 245:651-653(1989).
 RL [14]
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RP TISSUE=Brain;
 RX MEDLINE-87231971; PubMed:3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides";
 RA Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RL [15]
 RN SEQUENCE OF 286-366 FROM N.A.
 RP MEDLINE-88122640; PubMed:2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease";
 RA Nature 331:528-530(1988).
 RL [16]
 RN SEQUENCE OF 287-367 FROM N.A.
 RP MEDLINE-88122641; PubMed:2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity";
 RA Nature 331:530-532(1988).
 RL [17]
 RN SEQUENCE OF 507-770 FROM N.A.
 RP TISSUE=Brain Cortex;
 RX MEDLINE-88124954; PubMed:2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex";
 RA Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RL [18]
 RN SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RP MEDLINE-96139497; PubMed:8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I";
 RA J. Biol. Chem. 271:1613-1620(1996).
 RL [19]
 RN SEQUENCE OF 656-737 FROM N.A.
 RP MEDLINE-89392030; PubMed:2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor";
 RA Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RL [20]
 RN SEQUENCE OF 672-681.
 RP TISSUE=Brain cortex;
 RX MEDLINE-88035004; PubMed:3312495;
 RA Pardridge W.M., Vinters H.V., Fang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels";
 RA J. Neurochem. 49:1394-1401(1987).
 RL [21]
 RN SEQUENCE OF 674-770 FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE-87120328; PubMed:3810169;
 RA Goldsaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
 RT "Characterization and chromosomal localization of a cDNA encoding
 RT brain amyloid of Alzheimer's disease";

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Query Match      98.2%  Score 3585.5;  EB 1;  Length 770;
Best Local Similarity 90.0%;  Pred. No. 1.7c-17c;
Matches 693;  Conservative 1;  Mismatches 1;  Indels 75;  Gaps 1;

QY 1  MLPLGLALLLAANTARALEVPTDGNAGLLAEPQ-AMFCGRLNHMHNMVQNGKWDSPSGTK 60
DB 1  MLPLGLALLLAANTARALEVPTDGNAGLLAEPQAMFCGRLNHMHNMVQNGKWDSPSGTK 60

QY 61  TCIDTKEGILQCEVYVPELQITNVVEANOPVTIQNCKRGRKCKTHPHFVLPYRCLVG 120
DB 61  TCIDTKEGILQCEVYVPELQITNVVEANOPVTIQNCKRGRKCKTHPHFVLPYRCLVG 120

QY 121 EFVSALLVPDKCFHQRMDVCEHLLHMTVAKETCSEKSTKLHDYGMLLPCGADKFR 180
DB 121 EFVSALLVPDKCFHQRMDVCEHLLHMTVAKETCSEKSTKLHDYGMLLPCGADKFR 180

QY 181 GVEFVCCPLAESONVSADAEEDSDVWVGADIDVADGSEDKVWVAEEVAEVEE 240
DB 181 GVEFVCCPLAESONVSADAEEDSDVWVGADIDVADGSEDKVWVAEEVAEVEE 240

QY 241 EADDDDEDDGDEVEEAEFEYEATERTTSIATITTTTTSVEVEVVR----- 288
DB 241 EADDDDEDDGDEVEEAEFEYEATERTTSIATITTTTTSVEVEVVR----- 288

QY 289 ----- 288
DB 289 ----- 288

QY 301 RAMISRWFVTEGKCAPFFYGGCGGNRNFDTBEYCMVAGCSAMSSLLKTTQEP-LAR 360
DB 301 RAMISRWFVTEGKCAPFFYGGCGGNRNFDTBEYCMVAGCSAMSSLLKTTQEP-LAR 360

QY 289 ---VPTTAASPDAVDKYLETGPDENEHAFQKAKERLEAKHRERMSQVHREAEERQA 345
DB 361 PVKLDPTTAASPDAVDKYLETGPDENEHAFQKAKERLEAKHRERMSQVHREAEERQA 420

QY 346 KNLPRADKKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYTAL 405
DB 421 KNLPRADKKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYTAL 460

QY 406 QAVPRPRHVENMLKKYRAEKORQHTLKHFHVRVYDPKKAQIRSQVWTHLRVIYER 465
DB 481 QAVPRPRHVENMLKKYRAEKORQHTLKHFHVRVYDPKKAQIRSQVWTHLRVIYER 540

QY 466 MNQSLSLYNPVAAEE-QDEVELLQEQNYSDVLANMISEPRISYGNDAIMPSTET 525
DB 541 MNQSLSLYNPVAAEEIQDEVELLQEQNYSDVLANMISEPRISYGNDAIMPSTET 600

QY 526 KTTVELLVNGEFSLDLQPHHSTCADSVPAANTENEVEFPCARPAADRGLTTRPGSGLTN 585
DB 601 KTTVELLVNGEFSLDLQPHHSTCADSVPAANTENEVEFPCARPAADRGLTTRPGSGLTN 660

QY 586 IKTEISEVKMDAEFRHDSGYEVHQQKLVFFAEDVGSNKGAIIGLMVGGVVIAITVIFIL 645
DB 661 IKTEISEVKMDAEFRHDSGYEVHQQKLVFFAEDVGSNKGAIIGLMVGGVVIAITVIFIL 720

QY 646 VMLKKKQVTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFEQMN 695
DB 721 VMLKKKQVTSIHGGVVEVDAAVTPEERHLSKMQQNGYENPTYKFEQMN 770

RESULT 2
A4_MACFA
ID A4_MACFA STANDARD: PRT: 770 AA.
AC P53601; Q95KN7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-Ctf(59) (Gamma-secretase C-terminal fragment 59); Gamma-Ctf(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-Ctf(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.
```

```
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxId=9541;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC TISSUE=Cerebellum;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha Arpase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB family members, the APPA
CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPRLL1, APPB1, IBL, KNS2
CC (via its IPR domains) (By similarity), APPBP2 (via BASS) and DBP1.
CC In vitro, it binds MAP7 via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of A-P
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoId=P53601-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=P53601-2; Sequence=VSP_000010; VSP_000011;
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
```

CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/epsilon-catalin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42).
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and C-linked glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M58727; AAA36829.1; -;
 CC EMBL: M58726; AAA36828.1; -;
 CC HSSP: P05067; 1AAP.
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: Pf02177; A4_EXTRA; 1.
 CC Pfam: Pf03494; Beta_APP; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00759; BASICTPASE.
 CC ProDom: PD000222; Kunitz_BPTI; 1.
 CC SMART: SM00005; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 CC Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 CC Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 CC Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 CC Proteoglycan; Alternative splicing; Amyloid.
 CC SIGNAL 1 17 BY SIMILARITY.
 CC CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 CC CHAIN 18 667 SOLUBLE APP-ALPHA (POTENTIAL).
 CC CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 CC CHAIN 672 770 C99 (POTENTIAL).
 CC CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 CC CHAIN 672 712 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 CC CHAIN 688 770 C83 (POTENTIAL).
 CC CHAIN 688 713 P3(42) (POTENTIAL).
 CC CHAIN 688 711 P3(40) (POTENTIAL).

FT CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FT CHAIN	714	770	GAMMA-CTF(57) (POTENTIAL).
FT CHAIN	721	770	GAMMA-CTF(50) (POTENTIAL).
FT CHAIN	740	770	C31 (POTENTIAL).
FT DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	700	723	POTENTIAL.
FT DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	181	188	BPTI/KUNITZ INHIBITOR.
FT DOMAIN	291	341	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT DOMAIN	274	280	POLY-THR.
FT SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT SITE	671	672	CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
FT SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
FT SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
FT SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FT SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FT SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FT SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FT SITE	724	734	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT SITE	739	740	CLEAVAGE (BY CASPASES -3, -6, -8 OR -9) (BY SIMILARITY).
FT SITE	757	760	ENDOCYTOSIS SIGNAL.
FT SITE	759	762	NPXY MOTIF.

Query Match 98.2%; Score 3585.5; DB 1; Length 770;
 Best local Similarity 90.0%; Pred. No. 1.7e-170;
 Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;

QY	1	MLPGLALLLLA	AWTARALEVPTDGNAGLLAE	PTAMFCGRLLNMHNVQNGKWDSPGSK	60
DB	1	MLPGLALLLLA	AWTARALEVPTDGNAGLLAE	PTAMFCGRLLNMHNVQNGKWDSPGSK	60
QY	61	TCIDTKEGILQY	QCEVYPELQITNV	VEANQPVTONMCKRGKCKOCKTHPHFV	120
DB	61	TCIDTKEGILQY	QCEVYPELQITNV	VEANQPVTONMCKRGKCKOCKTHPHFV	120
QY	121	EFVSDALLVP	DKCKFLHQRMDVCETHL	WHVTAKETCSEKSTNLHDYGMLLPGIDKFR	180
DB	121	EFVSDALLVP	DKCKFLHQRMDVCETHL	WHVTAKETCSEKSTNLHDYGMLLPGIDKFR	180
QY	181	GVEFVCCPLAES	ONVDSADAEEDSDV	WMGADTDYADGSEDKVVEVAEEVEE	240
DB	181	GVEFVCCPLAES	ONVDSADAEEDSDV	WMGADTDYADGSEDKVVEVAEEVEE	240
QY	241	EADDEDEDEDE	DEVEEFAEPEEATERT	TSIAITTTTTTTSVEEVVVR	288
DB	241	EADDEDEDEDE	DEVEEFAEPEEATERT	TSIAITTTTTTTSVEEVVVR	288
QY	289	-----	-----	-----	288
DB	301	RAMISRWYFDV	TEGKCAFFYGGCGGN	NFNDETEYCNVCGSVMSOSLRKTTREPLTRD	350
QY	289	-----	-----	-----	345
DB	361	PVKLPTTAAS	TPDAVDKYLET	PGDENEHAHFQKAKERLEAKHRMSQVMREWEAE	420

QY 346 KNLPRADKKAVIQHFEQKVESLEQEAANEERQOLVETHMARVEAMLNDRRLAAENYIAL 405
 DB 421 KNLPRADKKAVIQHFEQKVESLEQEAANEERQOLVETHMARVEAMLNDRRLAAENYIAL 480
 QY 406 QAVPPRRHVNMLKAKYRAEOKDQHKLKHFHVRMYDPKKAQIRSQVWTHLVYIER 465
 DB 481 QAVPPRRHVNMLKAKYRAEOKDQHKLKHFHVRMYDPKKAQIRSQVWTHLVYIER 540
 QY 466 MNQSLSLYNNPAVAEIQDEVELQREQNYSDCVLANMKSEPAISYGNDAIMPSTJET 525
 DB 541 MNQSLSLYNNPAVAEIQDEVELQREQNYSDCVLANMKSEPAISYGNDAIMPSTJET 600
 QY 526 KTIIVLLPVGFEFSDLDLOPHSFQADSVDPANTENEVEPVDARPAADGLTTRGSGLTN 585
 DB 601 KTIIVLLPVGFEFSDLDLOPHSFQADSVDPANTENEVEPVDARPAADGLTTRGSGLTN 660
 QY 586 KTEIIEISEVKMDAERHDSGVYEHQKLVFFAEDVGSNKGKGIILGLWGVVIAIVVIL 645
 DB 661 KTEIIEISEVKMDAERHDSGVYEHQKLVFFAEDVGSNKGKGIILGLWGVVIAIVVIL 720
 QY 646 VMLKKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQKN 695
 DB 721 VMLKKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQKN 770
 RESULT 3
 AC-SAISC STANDARD: PRT: 751 AA.
 AC 095241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DE APP-beta (S-APP-beta); C59; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN APP
 OS Sahiari sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Anorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy.";
 RL Neurobiol Aging 16:805-808(1995).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APB1/p160 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metallated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPL1, APPP1, I81, KNS2
 CC (via its TPR domains) (By similarity). APPBP2 (via BASS) and DDB1.
 CC In vitro, it binds MAP2 via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized into endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
 CC nuclei of neurons (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing: Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=O95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=O95241-2; Sequence=Not described;
 CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-linked glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL: S81024; AAD14347.1; ..
HSSP: P05067; LAAP.
InterPro: IPR001868; A4_APP.
InterPro: IPR001255; Beta_APP.
InterPro: IPR002223; Kunitz_2_SF1.
Pfam: PF02177; A4_EXTRA; 1.
Pfam: PF03494; Beta_APP; 1.
Pfam: PF00014; Kunitz_2_SF1; 1.
PRINTS: PR00203; AMYLOIDA4.
PRINTS: PR00759; BASICPTASE.
PRODOM: PD000222; Kunitz_2_SF1; 1.
SMART: SM00005; A4_EXTRA; 1.
SMART: SM00131; KU; 1.
PROSITE: PS00319; A4_EXTRA; 1.
PROSITE: PS00320; A4_INTRA; 1.
PROSITE: PS00280; BPTI_KUNITZ_1; 1.
PROSITE: PS00279; BPTI_KUNITZ_2; 1.
Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
Coated pits; Neurons; Heparin-binding; Metal-binding; Copper; Iron;
Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
Proteoglycan; Amyloid; Alternative splicing.
SIGNAL 1 17 BY SIMILARITY.
CHAIN 18 751 A4 PROTEIN.
CHAIN 18 568 SOLUBLE APP-ALPHA (POTENTIAL).
CHAIN 18 552 SOLUBLE APP-BETA (POTENTIAL).
CHAIN 553 751 C99 (POTENTIAL).
CHAIN 553 694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
CHAIN 552 652 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
CHAIN 559 751 C83 (POTENTIAL).
CHAIN 559 694 P3(42) (POTENTIAL).
CHAIN 559 692 P3(40) (POTENTIAL).
CHAIN 551 751 GAMMA-C1F(59) (POTENTIAL).
CHAIN 551 751 GAMMA-C1F(57) (POTENTIAL).
CHAIN 551 751 GAMMA-C1F(50) (POTENTIAL).
CHAIN 721 751 C31 (POTENTIAL).
CHAIN 18 680 EXTRACELLULAR (POTENTIAL).
CHAIN 681 704 POTENTIAL.
CHAIN 705 751 CYTOPLASMIC (POTENTIAL).
CHAIN 110 751 HEPARIN-BINDING (BY SIMILARITY).
CHAIN 188 751 ZINC-BINDING (BY SIMILARITY).
CHAIN 291 341 BPTI/KUNITZ INHIBITOR.
CHAIN 316 344 HEPARIN-BINDING (BY SIMILARITY).
CHAIN 428 751 HEPARIN-BINDING (BY SIMILARITY).
CHAIN 504 521 COLLAGEN-BINDING (BY SIMILARITY).
CHAIN 713 732 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
DOMAIN 230 260 ASP/GLO-RICH (ACIDIC).
DOMAIN 274 280 POLY-THR.
DOMAIN 144 180 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
DOMAIN 302 302 REACTIVE BOND.
DOMAIN 652 653 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
SITE 653 654 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
SITE 669 669 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
SITE 685 685 INVOLVED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
SITE 687 687 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
SITE 692 693 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
SITE 694 695 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).

FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FT	SITE	705	715	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY CASPASES-3, -6, -8 OR -9) (BY SIMILARITY).
FT	SITE	738	741	ENDOCYTOSIS SIGNAL. (BY SIMILARITY).
FT	SITE	740	743	NPXY MOTIF.
FT	METAL	137	137	COPPER (BY SIMILARITY).
Query Match 98.0%; Score 3579; DB 1; Length 751;				
Best Local Similarity 91.9%; Pred No. 3, 4e-170;				
Matches 690; Conservative 2; Mismatches 3; Indels 56; Gaps 1;				
QY	1	MLPGIALLLA	AWTARA	LEVPTDGNAGLLAEPQIAMFCGRNLNHNHNQVNGKWDSDPGSTK 60
DB	1	MLPGIALLLA	AWTARA	LEVPTDGNAGLLAEPQIAMFCGRNLNHNHNQVNGKWDSDPGSTK 60
QY	61	TCIDTKEGIL	QCYEVY	PELOITINNVANQPVTIONCKRGKCKKTHPHFVIPYRCLVG 120
DB	61	TCIDTKEGIL	QCYEVY	PELOITINNVANQPVTIONCKRGKCKKTHPHFVIPYRCLVG 120
QY	121	EFVSDALL	VPDKCKFL	HOERMDVCETHLRHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB	121	EFVSDALL	VPDKCKFL	HOERMDVCETHLRHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
QY	181	GVEFVCCP	LAESDNDV	SADAEEDSDVWVGADIDYADGSEDKVVVEAEVEEAEVEE 240
DB	181	GVEFVCCP	LAESDNDV	SADAEEDSDVWVGADIDYADGSEDKVVVEAEVEEAEVEE 240
QY	241	EADDDDEDD	GDGEVEE	EAPEEYEAETRTSTATTTTTTTSVEEVVR----- 288
DB	241	EADDDDEDD	GDGEVEE	EAPEEYEAETRTSTATTTTTTTSVEEVVR----- 288
QY	289	-----	-----	-----VPTTAASIPDAVKYL 304
DB	301	RAHISRWY	FDVTEG	KCAPFFYGGCGGNRNFDTEEYCMAGCVSIPTTAASTPDAVKYL 360
QY	305	ETPGDENE	HAHFQK	AKERLEAKHREMSQVHWEAEERQAKNLPKADKAVIOHFQEKV 364
DB	361	ETPGDENE	HAHFQK	AKERLEAKHREMSQVHWEAEERQAKNLPKADKAVIOHFQEKV 420
QY	365	ESLEGEAAN	ERQCLV	ETHARVEAMLRRLALENYIALQAVPPRPHVFNMLKKYVR 424
DB	421	ESLEGEAAN	ERQCLV	ETHARVEAMLRRLALENYIALQAVPPRPHVFNMLKKYVR 480
QY	425	AEKORQHT	LKHFEH	RVMDPKKAAQIRSOVMTLRLVIERMNCISLLYNVPAVEIQ 484
DB	481	AEKORQHT	LKHFEH	RVMDPKKAAQIRSOVMTLRLVIERMNCISLLYNVPAVEIQ 540
QY	485	DEVDELLQ	KEQNYSD	VDVLANMISEPRISYGNDAIMPSTETKTIVVLLPVNGEFLDQLQ 544
DB	541	DEVDELLQ	KEQNYSD	VDVLANMISEPRISYGNDAIMPSTETKTIVVLLPVNGEFLDQLQ 600
QY	545	PWHSFGAD	SVDPANTE	NEVEPDARPAADRGTLTPRGSGLTNKTETEEISEVKMDAEFRHDS 604
DB	601	PWHSFGAD	SVDPANTE	NEVEPDARPAADRGTLTPRGSGLTNKTETEEISEVKMDAEFRHDS 660
QY	605	GVEVHQKL	VFFAEV	DVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGGVVEVD 564
DB	661	GVEVHQKL	VFFAEV	DVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGGVVEVD 720
QY	665	AAVTPEER	HLSKMQQ	NGYENPTYKFFEQMON 695
DB	721	AAVTPEER	HLSKMQQ	NGYENPTYKFFEQMON 751
RESULT 4				
A4_PIG STANDARD; PRT: 770 AA.				
ID A4_PIG AC P79307; Q29023; Q9TU10;				
DT 01-NOV-1997 (Rel. 35, Created)				
DT 15-SEP-2003 (Rel. 42, Last sequence update)				

DT 15-SEP-2003 (Rel. 42, last annotation update);
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(46);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 OS Secrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.;
 RT "Amyloid precursor protein 770.*";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RC TISSUE=Small intestine; N.A.
 RA Winteroe A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 667-723 FROM N.A.
 RC TISSUE=Brain;
 EX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through C-(11)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen 2 and IV (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IBL, KNS2
 CC (via its TPR domains) (By similarity). APPBP2 (via Bass) and DDB1
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of A-P
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clatherin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and

CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
 CC nuclei of neurons (By similarity).
 CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clatherin-mediated
 CC endocytosis (By similarity).
 CC -!- PM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides. S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
 CC similarity).
 CC -!- PM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PM: N- and O-linked glycosylated (By similarity).
 CC -!- PM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- PM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB032550; BAA84580.1; -
 CC EMBL; 284022; CAB06313.1; -
 CC EMBL; X56127; CA339592.1; -
 CC HSSP; P05067; JAAP.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR001255; Beta_APP.
 CC InterPro: IPR002223; Kunitz_BPT1.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC PRINTS: PR0203; AMYLOIDA4.
 CC PRINTS: PR00759; BASICPTASE.
 CC PRODom; PD000222; Kunitz_BPT1; 1.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPT1_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C59 (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 C83 (BY SIMILARITY).
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59).
 FT CHAIN 714 770 GAMMA-CTF(57).
 FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).
 FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).
 FT CHAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 120 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 135 155 COPPER-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPT1/KUNITZ INHIBITOR.
 FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 732 751 INTERACTION WITH G(C)-ALPHA (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
 Query Match 96.6%; Score 3530.5; DB 1; Length 770;
 Best Local Similarity 88.3%; Pred. No. 8.8e-158;
 Matches 680; Conservative 8; Mismatches 7; Indels 75; Gaps 1;
 QY 1 MLPGALLLAANTARALEVPTDGNAGLLAEPCIAECGRLNMNMVONGKWDSPSGTK 60
 DB 1 MLPGALLLAANTARALEVPTDGNAGLLAEPCIAECGRLNMNMVONGKWDSPSGTK 60
 QY 61 TCIDTREGILQYCOEYVPELQINNVYEAQPTVIONWCKRGRKQCKTHFPIYRCLVG 120
 DB 61 TCIDTREGILQYCOEYVPELQINNVYEAQPTVIONWCKRGRKQCKTHFPIYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHYVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHYVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNDVSDAEDDDSDVMWGGADTDYADGSDKVVVEAEVEAEVEE 240
 DB 181 GVEFVCCPLAESDNDVSDAEDDDSDVMWGGADTDYADGSDKVVVEAEVEAEVEE 240
 QY 241 EADDEDEDGDEVEEAEPEYEAERTTSTATTITTTTSSVEEVVYR----- 266
 DB 241 EADDEDEDGDEVEEAEPEYEAERTTSTATTITTTTSSVEEVVYR----- 266

DB 241 EADDEDEDGDEVEEAEPEYEAERTTSTATTITTTTSSVEEVVYR----- 300
 QY 289 ----- 288
 DB 301 RAMISRYFDVTEGKCAPFFYGGCGGNRNFDTEYCHAVCGSVMSQSLLIKTOEHLPOD 360
 QY 289 ---VPTTAASTDAVDKYLETFGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEARQA 345
 DB 361 PVKLPPTAASTDAVDKYLETFGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEARQA 420
 QY 346 KNLPKADKRAVLOHFOEKVESLEQEAANEEROLVETHMARVEAMLNDRRRLALENYITAL 405
 DB 421 KNLPKADKRAVLOHFOEKVESLEQEAANEEROLVETHMARVEAMLNDRRRLALENYITAL 480
 QY 406 QAVPPRPRIHVNNLKKYVRAEQDKROHTLKHFEHVMYVDPKKAQIRSOVTHLRVIYER 465
 DB 481 QAVPPRPRIHVNNLKKYVRAEQDKROHTLKHFEHVMYVDPKKAQIRSOVTHLRVIYER 540
 QY 466 MNQSLSLNYPVAVEEIQDEVDLLOKEQYSDOVLANMISEPRIISYGNALMPSLLET 525
 DB 541 MNQSLSLNYPVAVEEIQDEVDLLOKEQYSDOVLANMISEPRIISYGNALMPSLLET 600
 QY 526 KTIIVLLPVNGEFSLDLQPHWHSFGADSVPAANTEVEPVDARPAACRGITRRGSGLTN 585
 DB 601 KTIIVLLPVNGEFSLDLQPHWHSFGADSVPAANTEVEPVDARPAACRGITRRGSGLTN 660
 QY 586 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGVVIVITL 645
 DB 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGVVIVITL 720
 QY 646 VMLKKQYTSIIHGVVVEVDAAVTPPERHLKSKMQCQNGENPTYKFFEQMGN 695
 DB 721 VMLKKQYTSIIHGVVVEVDAAVTPPERHLKSKMQCQNGENPTYKFFEQMGN 770
 RESULT 5
 A4_CAVPO
 ID A4_CAVPO STANDARD; PRI: 770 AA.
 AC Q60495; Q60496;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31).
 GN APP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Mystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mceller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing."
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 RA Mao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta."
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;

RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA Bigl V.,
RT "Guinea-pig primary cell cultures provide a model to study expression
RT and amyloidogenic processing of endogenous amyloid precursor
RT protein.",
RL Neuroscience 95:243-254(2000).
RN [4]

RP GAMMA-SECRETASE PROCESSING.
RX MEDLINE-20576391; PubMed=11035007;
RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.,
RT "A novel gamma-secretase assay based on detection of the putative
RT C-terminal fragment-gamma of amyloid beta protein precursor.",
RL J. Biol. Chem. 276:431-487(2001).

CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(C) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metallated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC and apolipoproteins E and J in the CSF and to HDL particles in
CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC -!- FUNCTION: Apolipins elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain (By similarity).
CC -!- FUNCTION: The gamma-C9 peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Birds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB family members, the APPA
CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APPBPI, IBI, KNS2
CC (via its TPR domains). APPB2 (via BASS) and DDB1 (By similarity).
CC Associates with microtubules in the presence of ATP and in a
CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC the apoE4 isoform-beta-APP40 complex is capable of being
CC transported across the blood-brain barrier.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated pits
CC (By similarity). During maturation, the immature APP (N-
CC glycosylated in the endoplasmic reticulum) moves to the Golgi
CC complex where complete maturation occurs (O-glycosylated and
CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC APP is released into the extracellular space and the C-terminal is
CC internalized to endosomes and lysosomes (By similarity). Some APP
CC accumulates in secretory transport vesicles leaving the late Golgi
CC compartment and returns to the cell surface (By similarity). APP
CC sorts to the basolateral surface in epithelial cells (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms, missing exons 7,8 and 15, seem to
CC exist. The L-isoforms, missing exon 15, are referred to as
CC appicans;
CC Name=APP770;

CC IsoId=O60495-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=O60495-2; Sequence=VSP_007221, VSP_007222;
CC TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC brain. The longer isoforms containing the BPTI domain are
CC predominantly expressed in peripheral organs such as muscle and
CC liver.
CC -!- INDUCTION: Increased levels during neuronal differentiation.
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells.
CC -!- DOMAIN: The NPYX sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPYX motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue (By similarity). The NPYX site is also involved in
CC clathrin-mediated endocytosis.
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC gamma-secretase yields P3 peptides. This is the major secretory
CC pathway and is non-amyloidogenic. Alternatively,
CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC and amyloid-beta 42 (Abeta42), major components of amyloid
CC plaques, and the corresponding cytotoxic C-terminal fragments
CC (CTFs).
CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC apoptosis (By similarity).
CC -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC sulfate to the L-APP isoforms produces the APP proteoglycan core
CC proteins, the appicans (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific (By similarity).
CC Phosphorylation can affect APP processing, neuronal
CC differentiation and interaction with other proteins.
CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X97631; CAA56230.1; -;
CC EMBL: X99198; CAA67589.1; -;
CC HSSP: P05C67; 1BA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR008154; A4_extra.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF00014; Kunitz-BPTI; 1.
CC PRINTS: PR00203; AMYLOIDA4.
CC PRODOM: PD000222; Kunitz-BPTI; 1.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00131; KU; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS50279: BPTI_KUNITZ_2: 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neutrone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1 27
FT CHAIN 18 770
FT CHAIN 18 687
FT CHAIN 18 671
FT CHAIN 672 770
FT CHAIN 672 713
FT CHAIN 672 711
FT CHAIN 688 770
FT CHAIN 688 713
FT CHAIN 688 711
FT CHAIN 712 770
FT CHAIN 714 770
FT CHAIN 740 770

Query Match 96.3% Score 3517.5; DB 1; Length 770;
Best Local Similarity 88.1% Pred. No. 3.9e-167;
Matches 678; Conservative 7; Mismatches 10; Indels 75; Gaps 1;

QY 1 MLPGLALLIARATARA-LEVPDGNAGLLAEFO-AMFGRLNMHNNVQNKWSDPFGSK 60
DB 1 MLPGLALLIARATARA-LEVPDGNAGLLAEFO-AMFGRLNMHNNVQNKWSDPFGSK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQVPTONWCKRKRCKKTHPHFVPIYRCLVS 120
DB 61 TCIGSEKGLQYCOEYVPELQITNVVEANQVPTONWCKRKRCKKTHPHFVPIYRCLVS 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWTVAKECTSEKSTNLHGYMGLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWTVAKECTSEKSTNLHGYMGLPGIDKFR 180

QY 181 GVEFVCCPLAESDNDSDADAEEDSDVWVGGAUTDYADGSEDKVVEAEVEEVEEVEE 240
DB 181 GVEFVCCPLAESDNDSDADAEEDSDVWVGGAUTDYADGSEDKVVEAEVEEVEEVEE 240

QY 241 EADDDEDDGDEVEEAEPEEATEETTSIATTTTITTSVSEVVR- 265
DB 241 EADDDEDDGDEVEEAEPEEATEETTSIATTTTITTSVSEVVR- 265

QY 289 ---VPTIAASTPDADVCKYLETPGDNEHAHFQKAKERLEAKHREMSQVMEWEAEERQA 345
DB 361 PVKLPTIAASTPDADVCKYLETPGDNEHAHFQKAKERLEAKHREMSQVMEWEAEERQA 420

QY 346 KNLPKADKKAVIOHFQKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITAL 405
DB 421 KNLPKADKKAVIOHFQKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITAL 480

QY 406 QAVPPRPRHFNMLKYYVRAEOKDQHTLKHFEHVRMVDPKKAKOIRSOVMTLHVYER 465
DB 481 QAVPPRPRHFNMLKYYVRAEOKDQHTLKHFEHVRMVDPKKAKOIRSOVMTLHVYER 540

QY 466 MNGSLSLNVPAAVEEIODEYDELLQKEQNYSDSVLANMISEPRIISYGNDAIMPSTLET 525
DB 541 MNGSLSLNVPAAVEEIODEYDELLQKEQNYSDSVLANMISEPRIISYGNDAIMPSTLET 600

QY 526 KTTVELLPVNGEFLDDLPQPHSFADSVPAANTEVEFVDPARPAADRLTTRFGSGLTN 585
DB 601 KTTVELLPVNGEFLDDLPQPHSFADSVPAANTEVEFVDPARPAADRLTTRFGSGLTN 660

QY 586 IKTEEISEVKMDAEFRHDSGSEYVHOKLVFAEDVGSNKGAITIGLWGVGVVAFVPIETI 645
DB 661 IKTEEISEVKMDAEFRHDSGSEYVHOKLVFAEDVGSNKGAITIGLWGVGVVAFVPIETI 720

QY 646 VMLKKQYQY:SIHGGVVEYDAVTPERHLSKMQQNGYENPTYKFFEQMN 695
DB 646 VMLKKQYQY:SIHGGVVEYDAVTPERHLSKMQQNGYENPTYKFFEQMN 695

DB 721 VMLKKQYQY:SIHGGVVEYDAVTPERHLSKMQQNGYENPTYKFFEQMN 770

RESULT 6
A4_MOUSE STANDARD: PRT: 770 AA.
ID A4_MOUSE AC P12023; P97487; P97942; Q99K32;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE Soluble APP-alpha (S-APP-alpha); Amyloidogenic glycoprotein (AG) (Contains:
DE Soluble APP-beta (S-APP-beta); Soluble APP-beta (S-APP-beta); C99
DE (APP-C99); Beta-amyloid protein 42 (Beta-Ap42); Beta-amyloid protein
DE 40 (Beta-Ap40); C83; P3(42); P3(40); Gamma-Ctf(59) (Gamma-secretase
DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE (APP-C59); Gamma-Ctf(57) (Gamma-secretase C-terminal fragment 57)
DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-Ctf(50)
DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain:
DE 50) (AID(50)); C31].
GN APP.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322260;
RA Yamada T., Sakaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
R1 "Complementary DNA for the mouse homolog of the human amyloid beta
R1 protein precursor.";
R2 Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [2]
RP REVISIONS.
RA Yamada T.;
R2 Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
R1 "The amyloid beta protein precursor or proteinase nexin II from mouse
R1 is closer related to its human homolog than previously reported.";
R2 Biochim. Biophys. Acta 1129:141-143(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN=SAMP8; TISSUE=Hippocampus;
RX PubMed=11235921;
RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
R1 Alvarez J., Morley J.E.;
R2 "Molecular cloning, expression, and regulation of hippocampal amyloid
R2 precursor protein of senescence accelerated mouse (SAMP8).";
R3 Biochem. Cell Biol. 79:57-67(2001).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
R1 Sakai Y.;
R2 "Positive and negative regulatory elements for the expression of the
R2 Alzheimer's disease amyloid precursor-encoding gene in mouse.";
R3 Gene 112:189-195(1992).
RN [6]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R1 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.C.,
R2 A.Lschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R3 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R4 Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
R5 Sapliet M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
R6 Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loqueillano N.A., Peters G.J., Abramson R.D., Mullanah S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malick J.A., Gumaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton E., Kettunen M., Madan A., Young A.C., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield V.S.N., Krzyzinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein C.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903(2002).

RL [7]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING. TISSUE=Brain, and Kidney; MEDLINE=89149813; PubMed=2493250;

RX Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.; "Structure and expression of the alternatively-spliced forms of mRNA for the mouse homolog of Alzheimer's disease amyloid beta protein precursor"; Biochem. Biophys. Res. Commun. 158:906-912(1989).

RL [8]

RN SEQUENCE OF 656-737 FROM N.A.

RC STRAIN=129/Sv;

RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecechi M., Loring J.F., Goate A.M.; "Introduction of six mutations into the mouse genome using 'Hit and Run' gene-targeting: introduction of familial Alzheimer's disease mutations into the mouse amyloid precursor protein gene and humanization of the A-beta fragment."; Submitted (DEC-1996) to the ENBL/GenBank/DBJ databases.

RL [10]

RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS. PubMed=8510506;

RX Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.; "Regional distribution of the alternatively spliced isoforms of beta APP RNA transcript in the brain of normal, heterozygous and homozygous weaver mutant mice as revealed by in situ hybridization histochemistry."; Brain Res. Mol. Brain Res. 17:340-346(1993).

RL [11]

RP INTERACTION WITH KNS2. PubMed=1114335;

RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.; "Axonal transport of amyloid precursor protein is mediated by direct binding to the kinesin light chain subunit of kinesin-1."; Neuron 28:449-459(2000).

RL [12]

RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-726; THR-743; TYR-757; ASN-759 AND TYR-762. MEDLINE=21408156; PubMed=11517249;

RX Matsuda S., Yasukawa T., Homma Y., Ito Y., Nishikura T., Hiraki T., Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T., Kyriakis J.M., Nishimoto T.; "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1 scaffolds Alzheimer's amyloid precursor protein with JNK."; J. Neurosci. 21:6597-6607(2001).

RL [13]

RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION. MEDLINE=22028091; PubMed=15912189;

RX Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.; "Interaction of Alzheimer's beta-amyloid precursor family proteins with scaffold proteins of the JNK signaling cascade."; J. Biol. Chem. 277:20070-20078(2002).

RL [14]

RP INTERACTION OF CTF PEPTIDES WITH NUMB. PubMed=12011466;

RX Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A., Meucci O., McGrade J.C., Rakic P., Adamio L.; "The gamma-secretase-generated intracellular domain of beta-amyloid precursor protein binds Numb and inhibits Notch signaling."; Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).

RL [15]

RN GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1. PubMed=11553691;

RX Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.; "The amyloid precursor protein (APP)-cytoplasmic fragment generated by gamma-secretase is rapidly degraded but distributes partially in a nuclear fraction of neurons in culture."; Neurochem. 78:1168-1178(2001).

RL [16]

CC -I- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell motility and transcription regulation through protein-protein interactions. Can promote transcription activation through binding to APPB1/Tip60 and inhibit Notch signaling pathways such as those mediated by G10 and JIP. Inhibits G10 alpha Apase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1. May be involved in copper homeostasis/oxidative stress through copper ion reduction. Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

CC -I- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron. Rat and mouse beta-amyloid peptides bind only weakly transient metals and have little reducing activity due to substitutions of transient metal chelating residues. Beta-APP42 may activate mononuclear phagocytes in the brain and elicit inflammatory responses. Promotes both tau aggregation and TPK II-mediated phosphorylation (By similarity).

CC -I- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis.

CC -I- SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits its serine phosphorylation. Also interacts with GPCR-like protein BPP, FPR1, APPB1, Ibl, KNS2 (via its TPR domains), APPB2 (via BASS) and DDB1 (By similarity). In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity). Interacts, through a C-terminal domain, with GNAO1 (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid associates with HADH2 (By similarity).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.5%; Score 3488.5; DB 1; Length 770;
Best Local Similarity 87.7%; Pred. No. 1,1e-165;
Matches 675; Conservative 6; Mismatches 14; Indels 75; Gaps 1;

QY 1 MLPLGALLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNKWSDPSGK 60
DQ 1 MLPLSALLLLAAWTVRALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNKWSDPSGK 60
QY 61 TCIDTNEGILQYCEVPELQITNVYEAQNPVTIQNCKRGKQCKTHPRFVYPCLVG 120
DB 61 TCIGTNEGILQYCEVPELQITNVYEAQNPVTIQNCKRGKQCKTHIVIPACLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEFLHMHVTVAKETCSEKSTNLHSDYQMLLPCGIDKFR 180

Db	121	EFVSDALLVPDKCKFLHQRMDVCEETHLHWHYAKETCSKSTNLHDYGMLLPCCGDKFR	180	RP	SEQUENCE OF 289-364 FROM N.A.
Qy	181	GVEFVCCPLAESDNVSDAEDSDSVWVGADTDYADGSEDKVVEAEVEEVAEVEFE	240	RC	TISSUE=Liver;
Db	181	GVEFVCCPLAESDSVSDAEDSDSVWVGADTDYADGSEDKVVEAEVEEVAEVEFE	240	RX	MEDLINE=89183625; PubMed=2648331;
Qy	241	EADDEDEDGDEVEEAEPEEATERTTSIATTTTITTESVEEVR-----	288	RA	Kang J., Mueller-Hill B.;
Db	241	EADDEDEDGDEVEEAEPEEATERTTSIATTTTITTESVEEVR-----	288	RT	"The sequence of the two extra exons in rat preA4.;"
Qy	289	-----	288	RL	Nucleic Acids Res. 17:2130-2130(1989).
Db	301	RAMISRNYFDVTECKCV2FFVGGCGNRNFDTEYCMVCGSVSTOSI.LKTTSELPQD	360	RN	[3]
Qy	289	---VPTTAASPDVAVKYLETPGDENEHAHFQAKERLEAKHRFRMSQVNRWEAEARQA	345	RP	SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
Db	361	PKLPTTAASPDVAVKYLETPGDENEHAHFQAKERLEAKHRFRMSQVNRWEAEARQA	420	RX	PubMed=11483588;
Qy	346	KNLPKADKAVIQHFQSKVESLECEAANERQQLVETHHARVEAMLNDRRRLALENYIAL	425	RA	Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
Db	421	KNLPKADKAVIQHFQSKVESLECEAANERQQLVETHHARVEAMLNDRRRLALENYIAL	480	RT	"Distinct intramembrane cleavage of the beta-amyloid precursor protein family resembling gamma-secretase-like cleavage of Notch.;"
Qy	406	QAVPPRPHVFNMLKVVRAEQDKROHTLKHFEHVRVMDPKAAQIRSQVWTHLRYIER	455	RL	J. Biol. Chem. 276:35235-35238(2001).
Db	481	QAVPPRPHVFNMLKVVRAEQDKROHTLKHFEHVRVMDPKAAQIRSQVWTHLRYIER	540	RN	[4]
Qy	466	MNQSLSLLYNVPAVAEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMPSTJET	525	RP	ALTERNATIVE SPLICING.
Db	541	MNQSLSLLYNVPAVAEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMPSTJET	600	RX	PubMed=8624099;
Qy	526	KTTVELLPVNGEFLDDIQWHSFGADSVPAANTFNEVEPVDAKPAADRGLTTPGSGCTN	585	RA	Sandbrink R., Masters C.L., Beyreuther K.;
Db	601	KTTVELLPVNGEFLDDIQWHSFGADSVPAANTFNEVEPVDAKPAADRGLTTPGSGCTN	660	RT	"APP gene family. Alternative splicing generates functionally related isoforms.;"
Qy	586	IKTEISEVMKDAEFRHDSGVYEHQKLVFAEDVGSNGKGAIIIGLMVGGVZATVIFITL	645	RL	Ann. N.Y. Acad. Sci. 777:281-287(1996).
Db	661	IKTEISEVMKDAEFRHDSGVYEHQKLVFAEDVGSNGKGAIIIGLMVGGVZATVIFITL	720	RN	[5]
Qy	546	VMLKKKYOTSIHHGVVEVDAATVPEERHLSKMGQNGYENPTYKFFEQMON 665		RP	TISSUE SPECIFICITY OF APPICAN.
Db	721	VMLKKKYOTSIHHGVVEVDAATVPEERHLSKMGQNGYENPTYKFFEQMON 773		RX	PubMed=7744833;
RESULT 7				RA	Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
A4_RAT				RT	Mytilinou C., Margolis R.U., Robakis N.K.;
AC				RT	"The Alzheimer amyloid precursor proteoglycan (appican) is present in brain and is produced by astrocytes but not by neurons in primary
DT				RT	neural cultures.;"
DE				RL	J. Biol. Chem. 270:11839-11844(1995).
DE				RN	[6]
DE				RP	TISSUE SPECIFICITY OF ISOFORMS.
DE				RX	PubMed=8996834;
DE				RA	Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
DE				RT	"Expression of the APP gene family in brain cells, brain development
DE				RT	and aging.;"
DE				RL	Gerontology 43:119-131(1997).
DE				RN	[7]
DE				RP	INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
DE				RX	TYR-762
DE				RA	Katanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
DE				RT	Suzuki T., Nairn A.C., Greengard P.;
DE				RT	"A 127-kDa protein (UV-DB) binds to the cytoplasmic domain of the
DE				RL	Alzheimer's amyloid precursor protein.;"
DE				RN	J. Neurochem. 72:549-556(1999).
DE				RP	[8]
DE				RX	INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
DE				RA	Brouillet E., Tremblay A., Galanaud D., Volovitch M., Bouillot C.,
DE				RT	Valenza C., Prochiantz A., Allinquant B.;
DE				RT	"The amyloid precursor protein interacts with Gq heterotrimeric
DE				RT	protein within a cell compartment specialized in signal
DE				RL	transduction.;"
DE				RN	J. Neurosci. 19:1717-1727(1999).
DE				RP	[9]
DE				RX	CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
DE				RA	MEDLINE=95256193; PubMed=7737970;
DE				RT	Pangalos M.N., Efthymiopoulos S., Shioi J., Robakis N.K.;
DE				RT	"The chondroitin sulfate attachment site of appican is formed by
DE				RL	splicing out exon 15 of the amyloid precursor gene.;"
DE				RN	J. Biol. Chem. 270:10388-10391(1995).
DE				RP	[10]
DE				RX	BETA-AMYLOID METAL-BINDING.
DE				RA	Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
DE				RT	Scarpa R.C., CuaJungco M.P., Gray D.N., Lim J., Moir R.D., Ianzi R.E.,
DE				RT	Bush A.I.;
DE				RT	"The A beta peptide of Alzheimer's disease directly produces hydrogen
DE				RL	peroxide through metal ion reduction.;"
DE				RN	Biochemistry 38:7609-7616(1999).
DE				RP	[11]
DE				RX	BETA-AMYLOID ZINC BINDING.
DE				RT	MEDLINE=99343552; PubMed=10413512;

RA Liu S.T., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 RP GLY-704.
 RX PubMed:11959460;
 RA Kanski J., Varadarajan S., Aksanova M., Butterfield D.A.;
 RI "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX PubMed:9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
 RA Greengard P., Suzuki T.;
 RI "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain; and
 RT cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]
 RP PHOSPHORYLATION ON SER-730.
 RX PubMed:10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RI "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE:99274744; PubMed:10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RI "Role of phosphorylation of Alzheimer's amyloid precursor protein
 during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX PubMed:10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RI "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX PubMed:11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RI "Appican, the proteoglycan form of the amyloid precursor protein,
 contains chondroitin sulfate F in the repeating disaccharide region
 and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in
 cell mobility and transcription regulation through protein-protein
 interactions (By similarity). Can promote transcription activation
 through binding to APBB1/rip60 and inhibit Notch signaling through
 interaction with Numb (By similarity). Couples to apoptosis-
 inducing pathways such as those mediated by G(O) and Jip. Inhibits
 G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 mediating the axonal transport of beta-secretase and presenilin 1
 (By similarity). May be involved in copper homeostasis/oxidative
 stress through copper ion reduction. Can regulate neurite
 outgrowth through binding to components of the extracellular
 matrix such as heparin and collagen I and IV (By similarity). The
 splice isoforms that contain the BPTI domain possess protease
 inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPX II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPB family members, the APPA
 CC family, MAPK3ip1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPB1, IBL, KNS2
 CC (via its TPR domains), APPB2 (via BASS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC Query Match 95.5%; Score 3488.5; DB 1; Length 770;
 CC Best Local Similarity 87.5%; Pred. No. 1.1e-165;
 CC Matches 674; Conservative 8; Mismatches 13; Indels 75; Gaps 1;
 CC
 CC QY 1 MLPGLALLC-AAWTAFALEVPDTGNAGLLAEPOIAMFCGRLNNHNMVONCKWDSOPSGTK 60
 CC Db 1 MLPGLALLC-AAWTAFALEVPDTGNAGLLAEPOIAMFCGRLNNHNMVONCKWDSOPSGTK 60
 CC QY 61 TCIDTREGILQYCEVYPELQITNVVEANQPTVIONMCKRGKQCKTHPHFVPIYRCLVG 120
 CC Db 61 TCIDTREGILQYCEVYPELQITNVVEANQPTVIONMCKRGKQCKTHPHFVPIYRCLVG 120
 CC QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 CC Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 CC QY 181 GVEFVCCPLAESDNDVSDADEDDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 CC Db 181 GVEFVCCPLAESDSDSDADEDDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 CC QY 241 EADDEDEDDGEVEEEAEPEYEEATERTSTATTITTTTITTESVEEVYR----- 288
 CC Db 241 EADDEDEDDGEVEEEAEPEYEEATERTSTATTITTTTITTESVEEVYR----- 288
 CC QY 289 ----- 288
 CC Db 301 RAMISRWYFDVTGKCAPFFYGGCGGNRNFTDTEYCMVAGSVSSQLKTTSEPLPD 360
 CC QY 289 ---VPTIAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRKMSQVMEWEAEERQA 345
 CC Db 361 PVKLPPTAATPDAVDKYLETPGDENEHAHFQKAKERLEAKHRKMSQVMEWEAEERQA 420
 CC QY 346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEANLNDRRRLALENYITAL 405
 CC Db 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEANLNDRRRLALENYITAL 480
 CC QY 406 QAVPPRPRIHVNMLKKYVRAEQKDRQHTLKHFEHVRWDFPKAAQIRSQVMTLRIYIER 465
 CC Db 481 QAVPPRPRIHVNMLKKYVRAEQKDRQHTLKHFEHVRWDFPKAAQIRSQVMTLRIYIER 540
 CC QY 466 MNQSLLLYNPVPAVEEIQDEVDLLQKQNSDDVLANWISPRISYNDALMPSLTET 525
 CC Db 541 MNQSLLLYNPVPAVEEIQDEVDLLQKQNSDDVLANWISPRISYNDALMPSLTET 600
 CC QY 526 KTTVELLPVNGEFLDQLQPHWSFGADSVPAENTENEVEPVDARPAADRLITTPGSGLTN 585

Db 601 KTTVELLPVNGFSDJDLQPMHFGVDSVPANTENEVEVDARPAADRLT-RPGSGLTN 660
 Qy 586 IKTEEISEVKMDAEFRHDSGYEHHOKLVFAEDVGSNKGAIIGLMVGGWIAITVIFIL 645
 Db 661 IKTEEISEVKMDAEFGDSGFEYRHKLVFAEDVGSNKGAIIGLMVGGW-ATV-VIIL 720
 Qy 646 VMLKKKQYTSIHGGVVEVDAVTPPERHLSKMQQNGYENPTYKFFEQMON 695
 Db 721 VMLKKKQYTSIHGGVVEVDAVTPPERHLSKMQQNGYENPTYKFFEQMON 770

RESULT 8

APP2_MOUSE STANDARD: PRT: 695 AA.
 AC Q06335;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amyloid-like protein 2 precursor (CDEI-box binding protein); (CDEBP).
 GN APLP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Fetal brain;
 RA von der Kammer H.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 1-245 FROM N.A.
 RA MEDLIN=94032480; PubMed=8218408;
 RX Hanes J.; von der Kammer H.; Kristiansson G.I.; Scheit K.H.;
 RT "the complete cDNA coding sequence for the mouse CDEI binding
 protein.";
 RL Biochim. Biophys. Acta 1216:154-156(1993).
 [3]
 RP SEQUENCE OF 185-695 FROM N.A.
 RA MEDLINE=93129193; PubMed=1482349;
 RX Vidal F.; Blangy A.; Rassoulzadegan M.; Cuzin F.;
 RT "A murine sequence-specific DNA binding protein shows extensive local
 similarities to the amyloid precursor protein.";
 RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
 [4]
 RP SEQUENCE OF 1-35 FROM N.A.
 RA STRAIN=129/Sv;
 RX MEDLINE=96029629; PubMed=7592716;
 RA von Koch C.S.; Lahiri D.K.; Mammen A.L.; Copeland N.G.;
 RA Gilbert D.J.; Jenkins N.A.; Sisodia S.S.;
 RT "The mouse APLP2 gene. Chromosomal localization and promoter
 characterization.";
 RL J. Biol. Chem. 270:25475-25480(1995).
 CC -!- FUNCTION: BINDS TO THE DNA 5'-GTCACATG-3' (CDEI BOX) WHICH PLAYS
 CC AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
 CC (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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 CC -----
 DR EMBL; Z22592; CAA80306.1; .
 DR EMBL; M97216; AAC20039.1; .
 DR EMBL; U34291; AAC52318.1; .
 DR PIR; S38344; S38344.
 DR HSSP; P05067; LMP.

DR MGI:88047; APLP2.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PRO0203; AMYLOIDA4.
 DR SMART: SM0006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Transmembrane; DNA-binding; Signal; Nuclear protein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 695 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 624 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 625 648 POTENTIAL.
 FT DOMAIN 649 695 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 218 294 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 218 231 POLY-GLU.
 FT DOMAIN 256 266 POLY-GLU.
 FT DOMAIN 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 185 189 GMLP -> MACCC (IN REF. 3).
 SS SEQUENCE 695 AA: B9F4B95AAB2A0311 CRC64;
 Query Match 47.4%; Score 1730; DB 1; Length 695;
 Best Local Similarity 49.2%; Pred. No. 9.6e-79;
 Matches 359; Conservative 118; Mismatches 163; Indels 90; Gaps 19;
 Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPOIAMFCGRNLNMHMYQNGKWSDP 56
 Db 15 LLLLLLIGLTAPAAALAGYIEALAAAGTGFVAEPQIAMLGKGLNMHVNIQTCKWEPDP 74
 Qy 57 SGTKCIDTKGILQYQEVYFPELQITNVVEANQPTIQLNCKKGRKCKOCTHPHFVLPYR 116
 Db 75 TGTSCLTGTEVLYQCOEYFPELQITNVMEANQFVNIDSNCWRDKRCKCKS--HIVPFK 132
 Qy 117 CLVGEVSDALLVPCKCKELHQRMDVCETHLHHTVAKETCSKSNLNDYGLMPCGI 176
 Db 133 CLVGEFVSIVLVDPNCOFFHQERMEVCEKQRHHTLVKEACLTGLTLYSGMLPCGV 192
 Qy 177 DKFRGVEFVCCPLAE--ESDNVDSADAPEDSDVMVGADTDYADGSEDKVVEVAE---E 231
 Db 133 DQFHGIEYVCCPQTKTVDSSTMSKEFEFE-----DEEDEEDYLDKSEFPE 243
 Qy 232 FEVAEVEERAD-DDEDDGDFVEEAE-----EPYEEA-ERTTSIATTTTTTIES 282
 Db 244 ADLEDTFAADEDEEEVEEDVDYDFKGGDYNE--ENTEPSSSEGTISDKS 301
 Qy 283 VEEVVRVPTTAASTPDVADVKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAE 342
 Db 302 IVHDVKVPPIPLPTND-VDVYLETSDONEHARFQAKKEQLERHNRMDRVKKEWEAE 360
 Qy 343 RQAKNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYI 402
 Db 361 LQAKNLPIERTOTLIQHFQAMVKALEKAAEKKQQLVETHLARVEAMLNDRRR:ALENYL 420
 Qy 403 TALQAVPPRPRHFMMLKKYVRABQKQKRLTKHFHEVRVMDPKKAAQIRSQVTHLRVI 462
 Db 421 AALQSDPFRPHRIQLALRRYVRAENKRLHTRHQHVLAVDPEKAAQMSQVMTLHRVI 480
 Qy 463 YERNQSLLYNYPVAEEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIPLSL 522
 Db 481 EERNQSLTLKYVPYVAEQIEIDELLQEQ-----ADM-----DQFTSSI 523
 Qy 523 TETKTVTELLPVNGEFLDDLPWHSFGADSVPAANTEVEPVDARPAADRGTLTRPGSG 582
 Db 524 SENPVDVVRVSESE-EIPPEPPLHPF-----PSLSENE-----GSGMAEQD-G 566
 Qy 583 LTNIKTEEI-SEVKMDAEFRHDSGYEVHOKLVFAEDVGS-----NKK 624
 Db 567 LIGAEKVINSKNKNMKNWIDETLDV--KEMIFNAERVSGLEEEPEVSGPLREDFSLSS 624
 Qy 625 GAIIGLMVGGVVIATVITILVMLKKKQYTSIHGGVVEVDAVTPPERHLSKMQQNGYEN 684
 Db 625 NALIGLLVIAVIAITVIVISLVMLRKRYGTISHGIVEVDPMPLTPEERHLKMKQNGYEN 684
 Qy 685 PTYKFFEQMQ 694


```
Db      685 PTKYLQMQ 694
|||||
RESULT 9
APP2_HUMAN STANDARD:      PRT; 763 AA.
AC Q06481.1
DI 01-JUN-1994 (Rel. 29, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE (CDEI-box binding protein) (CDEB2).
GN APP2 OR APP2.2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93250009; PubMed=8485127;
RA Norris K., Foster D.C.;
RA "Molecular cloning of the cDNA for a human amyloid precursor protein
RA homolog: evidence for a multigene family.";
RL Biochemistry 32:4481-4486(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Hancs J., Klaudiny J., Scheit K.H.;
RA "A human amyloid precursor-like protein is highly homologous to a
RA mouse sequence-specific DNA-binding protein.";
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035131; PubMed=8220435;
RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA Hyman B.T., Neve R.L., Tanzi R.E.;
RA "Isolation and characterization of APLP2 encoding a homologue of the
RA Alzheimer's associated amyloid beta protein precursor.";
RL Nat. Genet. 5:95-99(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Lung;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Brat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hsieh S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Stevchenko Y., Bouffard G.G.,
RA Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.F.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length-h
RA human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC MAY BIND TO THE DNA 5'-GTACATG-3' (CDEI BOX).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
```

(POTENTIAL).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
Comment-Additional isoforms seem to exist:
Name=1;
IsoId=Q06481-1; Sequence=Displayed;
Name=2;
IsoId=Q06481-2; Sequence=VSP_000016;
Name=3;
IsoId=Q06481-3; Sequence=VSP_000019;
-!- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
AND ENDOTHELIAL TISSUES.
-!- SIMILARITY: BELONGS TO THE APP FAMILY
-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; S60099; AAC60589.1; -
EMBL; L09209; AAA35526.1; -
EMBL; 222572; CAA80295.1; -
EMBL; L27631; AAC41701.1; -
EMBL; BC000373; AAH00373.1; -
PIR; A49321; A49321.
HSSP; P05067; IIMP.
GeneW; HGNC:598; APLP2.
MIM; 104776; -
GO; GO:0016021; C: integral to membrane; NAS.
GO; GO:0005634; C: nucleus; IDA.
GO; GO:0003677; F: DNA binding activity; NAS.
GO; GO:0007186; P: G-protein coupled receptor protein signaling; NAS.
InterPro; IPR001868; A4_APP.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SM00006; A4_EXTRA; 1.
SMART; SM00331; KUT; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS0279; BPTI_KUNITZ_2; 1.
Transmembrane; Signal; Alternative splicing; DNA-binding;
Nuclear protein; Serine protease inhibitor.
SIGNAL 1 29 POTENTIAL.
CHAIN 30 763 AMYLOID-LIKE PROTEIN 2.
DOMAIN 30 692 EXTRACELLULAR (POTENTIAL).
TRANSMEM 693 716 POTENTIAL.
DOMAIN 717 763 CYTOPLASMIC (POTENTIAL).
DOMAIN 215 280 ASP/GLU-RICH (HIGHLY ACIDIC).
DOMAIN 306 364 BPTI/KUNITZ INHIBITOR.
DOMAIN 215 231 POLY-GLU.
ACT_SITE 320 321 REACTIVE BOND (BY SIMILARITY).
DISULFID 310 360 BY SIMILARITY.
DISULFID 319 343 BY SIMILARITY.
DISULFID 335 356 BY SIMILARITY.
VARSPPLIC 308 363 Missing (in isoform 2).
FT VARSPPLIC 613 624 /FTid=VSP_000018.
FT VARSPPLIC 543 543 Missing (in isoform 3).
FT CONFLICT 543 543 S -> I (IN REF. 1).
SQ SEQUENCE 763 AA; 86955 MW; CA3A7D6DDB8A28D0 CRC64;
Query Match 47.2%; Score 1723; DS 1; Length 763;
Best Local Similarity 47.0%; Pred. No. 2.4e-78;
Matches 371; Conservative 112; Mismatches 166; Indels 140; Gaps 20;

RA Read J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
 RA Bayer T.A., Multhaup G.,
 FT "Evidence for a copper-binding superfamily of the amyloid precursor
 FT protein.";
 RL Biochemistry 41:9310-9320(2000).
 CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, AβD1, activates transcription
 CC activation through APBβ1 (Fe65) binding (By similarity). Couples
 CC to JIP signal transduction through C-terminal binding. May
 CC interact with cellular G-protein signaling pathways. Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I.
 CC -!- FUNCTION: The gamma-CRF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPβ and AβA family members,
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
 CC localized to the postsynaptic density (PSD).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
 CC similarity).
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: O-glycosylated.
 CC -!- MISCCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC
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 DR EMBL: U48437; AAB96331.1; .
 DR EMBL: AD000864; AAB50173.1; .
 DR EMBL: BC012889; AAB12889.1; .
 DR HSP: P05067; LMWP.
 DR Genbank: HGNC:597; APLP1.
 DR MIM: 104775; .
 DR GO: GO:0005604; C:basement membrane; TAS.
 DR GO: GO:0005208; F:amyloid protein; TAS.
 DR GO: GO:0007397; P:histogenesis and organogenesis; TAS.
 DR GO: GO:0007399; P:neurogenesis; TAS.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PF00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 38
 FT CHAIN 39 650
 FT CHAIN 621 650
 FT DOMAIN 39 580
 FT TRANSMEM 581 603
 FT POTENTIAL 604 650
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 158 178
 FT DOMAIN 204 211
 FT ZINC-BINDING.

FI	DOMAIN	310	342	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	410	441	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	442	459	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	640	643	CLATHRIN-BINDING (POTENTIAL).
FT	DOMAIN	241	247	POLY-GLU.
FT	DOMAIN	264	268	REQUIRED FOR COPPER(II) REDUCTION (BY
FT	SITE	167	167	SIMILARITY).
FT	SITE	604	615	RASOLATERAL SORTING SIGNAL (BY
FT	SITE	620	621	SIMILARITY).
FT	SITE	638	641	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	640	643	ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT	CARBOHYD	337	337	NPXY MOTIF.
FT	CARBOHYD	461	461	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	461	461	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	551	551	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CONFLICT	48	48	A -> P (IN REF. 1).
SO	SEQUENCE	650 AA	72176 MW	B95F0F4DIC5BAC7 CRC64;

Query Match 32.4%; Score 1185; DB 1; Length 650;
 Best Local Similarity 38.7%; Pred. No. 8.2e-52;
 Matches 271; Conservative 115; Mismatches 231; Indels 84; Gaps 16;

QY	1	MLPGLALLLAAWTA	LEVT	DGNAGLLAE	POIA	MFCCGLRM	VMNVQNGK	WSDSPG	STK	60
DB	23	LPPLLLSLRAQPA	IGSLAGG	SGAAEAP	GSQAQV	AGLCGR	LTLLHRD	RTGRWEP	DPQSR	82
QY	61	TCIDTKEGILQY	COEYVPE	LOITV	VEANQ	PIVION	CKRKCK	ROCK	THPH	119
DB	83	RCLRPQVRLEY	CROMY	PELOI	ARVEQ	ATQAI	PMRMC	GGSRSG	SCARH	142
QY	120	GEFVSDALLVP	DKKFLH	QERD	YVCET	HLHWH	TVAKET	CTSEK	SLNHDY	179
DB	143	GEFVSEALLVP	EGCRFL	HQERMD	QCES	STRR	HQEAQ	ECAC	SSQGLH	202
QY	180	RGVEVCCPLAE	ESONVDS	ADAE	EDDS	VDWNG	ADIDY	ADGSE	DKVVEV	239
DB	203	REVEIVCCPP	PGTDP	--	PSGTAV	GDPS	TRSW	-----	PTGSR	246
QY	240	EEADDDDC	--	EDSDE	VEEAF	EPYEE	ATER	TTTAT	TTTTT	297
DB	247	ESFPQVDY	VEPPEA	EE	--	ETVPP	SSHT	LA	VGVK	291
QY	298	DAVDKYLTP	GDENH	AIHFQ	AKER	LEAK	HRMSQ	VMREWE	AEAK	357
DB	292	GVVDIYFC	MPGE	ISEH	EGFL	RAKMD	LEERR	MRQI	NEVRE	351
QY	358	QHFQEKVES	LEBOE	ANRQ	OLVET	HMAR	VEAM	LDRGR	LALEN	417
DB	352	EHFQILQ	TL	EEQVSG	ERQ	RLVET	HAT	RVIAL	INDQ	411
QY	418	MLKTYRAEQ	KDRQ	HTLKH	FHVR	MVDP	KAAQ	IRSO	VMTH	477
DB	412	ALRRYLRAE	QEQH	TLRH	YQHV	AAVDP	EKAQ	QMR	FQVHT	471
QY	478	AVAEIODE	VELLQ	KEQNY	SDDV	LANNI	SEPR	ISY	NDAL	537
DB	472	RLAQELR	FQI	ELLH	SEH	-----	LGP	SELA	-----	502
QY	538	FSLD	--	DLQ	PMH	SFC	ADSV	PANT	ENE	595
DB	503	SSEDKG	GLQ	PPDS	--	KDQ	TPN	-----	TL	547
QY	596	MDAE	FRHDS	QYEV	HH	--	QKLV	FA	EDV	651
DB	548	RKVNAS	VPRG	FPFH	SS	EQ	DEL	AP	AGT	607
QY	652	OYTS	IHHG	VVE	DA	AVT	TEER	HL	SKMQ	692
DB	608	PYGA	ISHG	VVE	VD	PML	TLE	EQ	QLR	648

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APPI_MOUSE
IC APPI_MOUSE STANDARD: PRT: 653 AA.
AC Q03157: Q8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
OS APPL1.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93066322; PubMed=1279593;
RA Wasco W., Bupp K., Magendanz M., Gusella J.F., Tanzi R.E.,
RA Solomon F.;
RA "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bossak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Plakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RN [3]
RP COLLAGEN-BINDING.
RX MEDLINE=96139497; PubMed=8576160;
RA Behr D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RI mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [4]
RP INTERACTION WITH DAB1.
RX MEDLINE=99389880; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT protein 1.";
RL J. Neurosci. 19:7507-7515(1999).
RN [5]
RP INTERACTION WITH MAPK8IP1.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/isllet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [6]
RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
RP TYR-641.
RX MEDLINE=22313598; PubMed=12228233;
RA Scheinfeld M.H., Gheris E., Laky K., Fowlkes B.J., D'Adamo L.;

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RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT secretase regulates transcription.";
RL J. Biol. Chem. 277:44195-44201(2002).
CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALD1, activates transcription
CC activation through APBB1 (Fe65) binding. Couples to JIP signal
CC transduction through C-terminal binding. May interact with
CC cellular G-protein signaling pathways. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I.
CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB and APPA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clathrin-mediated
CC endocytosis.
CC -!- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC similarity).
CC -!- PTM: N-glycosylated.
CC -!- PTM: O-glycosylated.
CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L04538; AAA37247.1; -.
DR EMBL: BC021877; AAH21877.1; -.
DR PIR: A46362; A46362.
DR HSP: P05066; LMWP.
DR MGD: MG1:88046; Appl1.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR KX Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW Glycoprotein.
FT SIGNAL 1 37 POTENTIAL
FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
FT CHAIN 624 653 C30 (BY SIMILARITY).
FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 606 POTENTIAL.
FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 157 177 COPPER-BINDING.
FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 263 271 POLY-GLU.
FT DOMAIN 535 538 POLY-SER.
FT DOMAIN 601 606 POLY-LEU.
FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
FT SIMILARITY).
FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY

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D5      6 LMIGLIPILVA-TVYAFSGSPAGSKRHEKFTPMVAFSGYRQYX-TEEGSNKTDDERYA 63
QY      61 TCIDTKSGILOYCEVYPELOIINVVEANQVNTIONWCKRGRKCKTHPHFVYPRCIAG 120
DB      64 7CFSGKDLKRCYKAYPSMNTITNIVEYSHSVSDMCREEGSPCK-WHSVRVYHCIDG 122
QY      121 EFVSDALLVPDKKFLHOERMDVCFTHLHWHHTVAKETCSRSKSN-----LEDYGMLLPC 174
DB      123 EFHEALQVPHDCQFQSHVNSRQNDYOHVWKEAGCKCTKSKGNKMDMYRSFAVLEFC 192
QY      175 GIDKFRGVEFYCCPLAEESUNVSDADEEDSDVMWGGCACTDYADGSEDKVVVEAEFEV 234
DB      183 ALDMFTGVFEVCCP-----NDQINTKDQKIK----- 209
QY      235 AEVVEEEADDEDEDGDEVEEAEAEPEEATERITSANTITTTTSVSEVVRVPTAA 294
DB      210 ---EDEDDEDDDEYEDDYSEEDKDEE----- 236
QY      295 STPOAVDKYLETPGDENEHAHFOKAKERLEAKHREMSOVMEEEA-----ERCAKNLP 349
DB      237 -EPSQDPYFKIANWINEHDDFKAEEMDEKHKRKYDKVMKEGCDLETRYNEQKAKD-P 294
QY      350 KADKAVIQ---HFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL- 405
DB      295 KGAEFKSOMNARFQKTVSSLEEEHKKRMKEIEAVHEERVOAMLNKKRCDATHYRQALA 354
QY      406 -QAVPPRPRHVENMLKKYVRAEQDROHTLKHFEHVRVMDPKKAAQIRSQVTHLRYIE 464
DB      355 THVKNPKHVSQSLKATIRAEKDRMHLNRYRHLKADSKAEAAAYKPTVIHLRYIDL 414
QY      465 RMNOSLSLLYNP-----AVA--BEIQDEVDLLOKQSNYSDDVLANMISEPRISY 513
DB      415 RINGTLAMLRDPDLKRYVPIATYKDYRDEYSPDISVE-----DSELTPIIHCDPFSK 470
QY      514 GN--DALMPSLT-----EKTQTVELLPVNGESLDLOQPHHFGADSPVANT---ENEVEP 564
DB      471 NAKLDVKAPTTTAKPVKETDNAKVLPTBASDSEEEADEYDEDEQVKKTPDKKKVKV 530
QY      565 VDARP-----AADRLITRPGSLNINIKTEE-----ISEVKMDA 598
DB      531 VDIPKEIKVTIEBEKAKPIVETSVQTDDEDEDESSSTSSSEDEDEKNIKELRVDI 590
QY      599 E-----FRHDSGYEVHHQKLVFFAEADYGSNGKGAIGLWGVGVVIATVIFITIVMLK 649
DB      591 EPIIDEPASFYRD-----KLQISPEVERSSVFPQVVLASANKFITAICIIAFAIT 642
QY      650 KKQYTSIHGVVEYDAAVTPPERILSKNQQNGYENPTYKFE 691
DB      643 NARRRRMRGFIYVD-VYTPBEHVAGQVNGYENPTYSEFD 693

RESULT 14
A4_DROME
ID A4_DROME STANDARD: PRT: 897 AA.
AC P14599; Q9TVVC; Q9U4H3; Q9W5F.;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-amyloid-like protein precursor.
GN APPL OR VND OR BCDNA:GH04413 OR EG:65F1.5 OR CG7727.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachyoptera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184650; PubMed=2494667;
RA Rosen D.R., Martin-Norris L., Luo L., White K.;
RT "A Drosophila gene encoding a protein resembling the human
RL beta-amyloid protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yeaman M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Baliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Fertaz C., Fertiera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J.J., Ye R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RN REVISIONS.
RP STRAIN=Berkeley;
RC MEDLINE=22436069; PubMed=12537572;
RA Hsira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradschky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.C.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RN SEQUENCE FROM N.A.
RP STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=107311137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster.";
RL Science 287:2220-2222(2000).
RN [5]
```

RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Ovary;
RX MEDLINE=20196012; PubMed=10731138;
RA Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
RA Stapleton M., Harvey D.A.;
RT "A Drosophila complementary DNA resource";
RN Science 287:2222-2224(2000).
[61]
RP SEQUENCE OF 1-83 FROM N.A.
RX MEDLINE=91184006; PubMed=2127912;
RA Martin-Morris L.E., White K.;
RT "The Drosophila transcript encoded by the beta-amyloid protein
precursor-like gene is restricted to the nervous system";
RL Development 110:185-193(1990).
CC !- FUNCTION: Probably corresponds to the protein encoded by the
essential locus vnd, a gene required for embryonic nervous system
development.
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- TISSUE SPECIFICITY: Expressed in post-mitotic neurons in the
central and peripheral nervous systems. Within the nervous system
transcripts are not observed in neuroblasts, newly generated
neurons and at least one class of presumed glial cells.
CC !- DEVELOPMENTAL STAGE: Expressed in all developmental stages.
CC !- DOMAIN: The clathrin-binding site is essential for its association
with α -tubulin, β -tubulin, and γ -tubulin. The sequence specific
recognition extends to peptide residues that are C-terminal to the
NPXY motif. This interaction appears to be independent of
phosphorylation (By similarity).
CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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DR EMBL: J04516; AAA28874.1; .
DR EMBL: AE003418; AAF45520.2; .
DR EMBL: AL031883; CAA21409.1; .
DR EMBL: AL022139; CAA21409.1; JOINED.
DR EMBL: AL022139; CAA18093.1; .
DR EMBL: AL031883; CAA18093.1; JOINED.
DR EMBL: AF181628; AAD55414.1; .
DR EMBL: X55774; CAA39294.1; .
DR EMBL: X55775; CAA39294.1; JOINED.
DR PIR: A32758; A32758.
DR HSP: P05067; IMWP.
DR FlyBase: FBgn000108; Appl.
DR GO: GO:0005576; C:extracellular; IDA.
DR GO: GO:0005886; C:plasma membrane; IDA.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Signal; Transmembrane; Amyloid; Neurogenesis.
FT SIGNAL 1 27
FT CHAIN 28 887
FT DOMAIN 28 813
FT TRANSMEM 814 834
FT DOMAIN 835 887
FT DOMAIN 877 880
FT CARBOHYD 150 150
FT CARBOHYD 161 161
FT CARBOHYD 237 237
FT CARBOHYD 240 240
FT CARBOHYD 574 574
FT CONFLICT 177 177
FT CONFLICT 229 229
FT CONFLICT 332 332
FT CONFLICT 743 743

SQ	SEQUENCE	887 AA:	98332 MW:	FOF0855AD65A5275 CRC64;
	Query Match	20.7%	Score 755.5;	DB 1; Length 887;
	Best Local Similarity	25.6%	Pred. No. 2.1e-30;	
	Matches 234;	Conservative 128;	Mismatches 286;	Indels 265; Gaps 29;
QY	7 LLLLAANTARALEVPTDGNAGLLA-----EFOIAMFC--GRLNHMHVY-QNGKNDSDPSG	58		
DB	9 LLLRLSLVVLAI-----GTAQVQAASPRWEPQIAVLCEAGQIQYQVYLSSEGRWVTLDSK	63		
QY	59 T---KTCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONKCKRG---RKCKTHPEFV	112		
DB	64 KTGTGTCCLDKMDLLDYCKKAYPNRDIINIVESSHYQVIGCWCRQGALNAAKCKGSRHWI	123		
QY	113 IPYRCVLSEFVSALLVPDKCKFLHQMERMVCEYTHLHWHITVAKETCSEKSTNLHIDYGMLL	172		
DB	124 KPFRCCL-GPFSODALLVPEGCLFDHINASHKCPVPRVWNTGTAAACQERGMQMRSPFAMLL	182		
QY	173 PCGIDKFCRCVPEVCCP-----LAESDNDV---S	198		
DB	183 PCGISVFCSEVFCVCCPKHFKTDEIHVKKTDLPVMPAAOINSADEIVNDEEDSDNSNYS	242		
QY	199 ADAEEDSDVMWGGADTDYADGSEDKVVEVAEEV-----AE	236		
DB	243 KDAEEDDLG-----DEDDLMGDDDEDDMWADENATAGGSPNTSSGSDNSGSLDDINAE	296		
QY	237 VEE-EEACDDEDEDCDEVEEAEFV-----EATER	268		
DB	297 YDSGEEDNYEEDGAGSEAEVEASWDQSGAKVVSLSKSSSPSSAPVAPAEKAPVK	356		
QY	269 TTSIATTTTTFESVEEV-----RVPTTAATSTDAVKYLETPTGDENEHAHEQ	317		
DB	357 SESVTSTPOLSASAAFAVAANSNGSGTGAGAPPSTAQPTS---DRYTFHDPHYEQSYK	413		
QY	318 KAKERLEAKHREMSQVREWEAEERQAKNLPKADKKA-----VIOHFEKYESELEQE	370		
DB	414 VSKRLESHREKTRVNMKOWSDLEEKYODMRADPKAAQSFQKQRTARFOTISQVQALEEE	473		
QY	371 AANEQQLVETHMARVAMLNDRRLALENYITALQAVPPRPRHVFNNLKKRYRAEQKDR	430		
DB	474 GNAEKHOLAAMHQORVLAHINQKREAMTCYTQALTQFPNNAHHVEKCLQKLLRALHDKDR	533		
QY	431 QHTLKHFEH-VRMVDP---KKAQIRSQVMTHLRVYERMNQSLSLINVPVAVAEFI----	483		
DB	534 AHALAHYRLHNSGGPGGGLGGLAAASERPTLERLIDIRAVNQSMITMLKRYPELSAKIAQL	593		
QY	484 -----QDEV-----	487		
DB	594 MNDYILALRSKDDIFGSSLGMSSEAEAGILDKYRVELEKRYVAEKERLAEKQKQRAA	653		
QY	488 -----DELLOKEQNYSDVLANMISE-----PRISYGNDAI	518		
DB	654 EREKLEERLEAKKVDMDLMSQVAAOSQPTSTOSQAOQOQOQKSLPCKELGPDA	713		
QY	519 M-----PSLTETKTIVELLPVNGEFLSDLOPHWFSFGADSVPAANTEVEVPDARPADR	573		
DB	714 LVTAANPNLETTKS-----FKDLSDE-----YGEATVSSSTKVQTVLPTVDDDAVQR	760		
QY	574 GLTTRPGSGLTNKTETEEISEVKMDAEFRHDSGYEYHOKLVF-----FAEDVGSNK---G	625		
DB	761 AVEDVAAA-----VAHQEAEPQVOHFMTDHLGHRSSFSLRREFQAQHAHAKEGRN	811		
QY	626 AIGLMVGGVIATVIFITLVMKKQYTSIH-HGVVEVDAVTP-----EERHLSKMQ	678		
DB	812 VYFTLSFAGIALMAAVFVGAVAKWRTSRSPHAQFIEVDQNVVTHHPIVREKIVPNNQ	871		
QY	679 QNCYENPTYKFFE	691		
DB	872 INGYENPTYKFFE	884		

RESULT 15
A4_BOVIN


```

ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2003 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta); (Fragment)].
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC T-SSUE-Brain;
RX MEDLINE=9201709; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X56124; CAA39589.1; .
CC EMBL: X56126; CAA39591.1; .
CC HSSP: P05067; IBA4.
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF03494; Beta-APP; 1.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
KW NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59
SQ SEQUENCE 59 AA: 6414 MW: 743469D488A2E12D CRC64;

Query Match 7.98; Score 287; DB 1; Length 59;
Best Local Similarity 98.3%; Pred. No. 1.2e-06;
Matches 58; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 591 ISEVKMDAEFRHDSGYEHVKLVFFAEEDVGSNKGAIIGLMVGGVIATVITLVMLK 649
      |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 1 ISEVKMDAEFRHDSGYEHVKLVFFAEEDVGSNKGAIIGLMVGGVIATVITLVMLK 59

Search completed: October 2, 2003, 13:59:43
Job time : 14 secs
```

GenCore version 5.1.6
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QM protein: - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 39 Seconds

(without alignments)
4611.863 Million cell updates/sec

Title: US-09-806-194-20

Perfect score: 3653

Sequence: 1 MLPGLALLLAANTARALEV.....QQNGYENPTYKFFQMAKNK 597

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3568	97.7	695	11	O60496 cavia sp. p
2	3535	96.8	695	11	P97487 mus musculus
3	3530.5	96.6	770	6	Q9T010 sus scrofa
4	3423	93.7	695	13	Q9DGJ8 gallus gall
5	3382	92.6	751	13	Q9DGJ7 gallus gall
6	3209	87.8	693	13	Q98SC0 xenopus lae
7	3185	87.2	695	13	Q98SF9 xenopus lae
8	3098	84.8	747	13	Q91963 xenopus lae
9	2959.5	81.0	699	13	Q57394 narke japon
10	2762.5	75.6	569	13	Q9PVL1 gallus gall
11	2630.5	72.0	607	11	Q99K32 mus musculus
12	2608	71.4	534	13	Q93296 gallus gall
13	2568	70.3	780	13	Q73683 tetraodon f
14	2524	69.1	738	13	Q90W28 brachydanio
15	2482.5	68.0	694	13	O8UUR9 brachydanio
16	2443.5	66.9	737	13	O93279 fugu rubrip

ALIGNMENTS

RESULT 1

O60496 PRELIMINARY; PRT: 695 AA.

AC O60496; (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-01-2002 (TREMELREL. 22, Last annotation update)
 DE Putative amyloid precursor protein.
 OS Cavia sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CX NCBI_TaxID:10143;
 RN 11
 PP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RT Amyloid precursor protein in Guinea pigs - complete cDNA sequence and alternative splicing.;
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 DR EMBL; X97631; CAA66230.1; .
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SO SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match: 97.7%; Score 3568; DB 11; Length 695;

Best Local Similarity 97.7%; Pred. No. 6.1e-208;
 Matches 679; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Oy 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNNHNVQNGKWDSPSGTK 60

Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNNHNVQNGKWDSPSGTK 60

Q919E7 brachydanio
 Q8BPC7 mus musculus
 Q13861 homo sapien
 Q14662 homo sapien
 Q64348 mus musculu
 Q61482 mus musculu
 Q86709 mus musculu
 Q8AUS0 brachydanio
 Q8AUI8 brachydanio
 Q9BT36 homo sapien
 Q8BPV5 mus musculu
 Q14594 homo sapien
 Q8AUI7 brachydanio
 P79307 sus scrofa
 Q9JH58 chelydra se
 Q9CYS4 mus musculu
 Q28673 oryctolagus
 Q16014 homo sapien
 Q16019 homo sapien
 Q16020 homo sapien
 Q35463 cricetus
 Q9QZ78 cavia sp. p
 O8R0R7 mus musculu
 Q97917 bos taurus
 Q96T47 drosophila
 Q9V628 drosophila
 Q9S593 drosophila
 Q91255 petromyzon
 Q9V719 drosophila

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGKCKKTHPHFVTPRCVLS 120
DB 61 TCIGSGEGILQYCOEYVPELQITNVVEANOPVTIQNMCKRSRKCKKTHPHFVTPRCVLS 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEAEPTSTATTITTTESVEEVEVVRVPTTAASPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEEAEPTSTATTITTTESVEEVEVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
QY 361 QKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAOAVPPRPHVFNMLK 420
DB 361 QKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAOAVPPRPHVFNMLK 420
QY 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLYNVPVA 480
DB 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLYNVPVA 480
QY 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTITKTITVELLPVNGEFSL 540
DB 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTITKTITVELLPVNGEFSL 540
QY 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGULTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGULTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660
DB 601 RHDGSEYVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660

RESULT 2

P97487
ID P97487 PRELIMINARY: PRT: 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hippocampal amyloid protein.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=Hippocampus;
RA Flood J.F., Kumar V.B., Sasser I., Word I., Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=129SV;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capocchi M.,
RA Loring J.F., Goate A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U840.2; AAB41502.1; -;
DR EMBL: U82624; AAB40919.1; -;
DR HSSP: P05067; 1MWP.

LR MG: 88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PFC2177; A4_EXTRA; 1.
DR Pfam: PFC3494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match
Best Local Similarity 97.1%; Score 3535; DB 11; Length 695;
Matches 675; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPQIAFMFCGRNLNMHNMVNGKWDSPGSK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPQIAFMFCGRNLNMHNMVNGKWDSPGSK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGKCKKTHPHFVTPRCVLS 120
DB 61 TCIGSGEGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGKCKKTHPHFVTPRCVLS 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEAEPTSTATTITTTESVEEVEVVRVPTTAASPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEEAEPTSTATTITTTESVEEVEVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
QY 361 QKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAOAVPPRPHVFNMLK 420
DB 361 QKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAOAVPPRPHVFNMLK 420
QY 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLYNVPVA 480
DB 421 KYVRAEQDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLYNVPVA 480
QY 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTITKTITVELLPVNGEFSL 540
DB 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTITKTITVELLPVNGEFSL 540
QY 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGULTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGULTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660
DB 601 RHDGSEYVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660
QY 661 VEVDAAVTPRPHLSKMOONGYENPTYKFFEQMKN 695
DB 661 VEVDAAVTPRPHLSKMOONGYENPTYKFFEQMKN 695

RESULT 3

Q9TUI0
ID Q9TUI0 PRELIMINARY: PRT: 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Amyloid precursor protein.
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN NCBI_TaxID=9823;
[1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAA84580.1;
DR HSSP; P05067; IAAp.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00614; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00305; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5f7a1dcb2bcc583e CRC64;

Query Match 96.6%; Score 3530.5; DB 6; Length 770;
Best Local Similarity 88.3%; Pred. No. 1.3e+205;
Matches 680; Conservative 8; Mismatches 7; Indels 75; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONWCKGRKCKOCTHHPFVYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONWCKGRKCKOCTHHPFVYRCVLG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNLJPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNLJPCGIDKFR 180

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNLJPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNLJPCGIDKFR 180

QY 181 GFVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GFVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEAEVEE 240

QY 241 FAEDDEDEDGDEVEEAEPYEATERTTSIATTTTTTIESVEEYVVR----- 288
DB 241 FAEDDEDEDGDEVEEAEPYEATERTTSIATTTTTTIESVEEYVVR----- 288

QY 289 ----- 286
DB 289 ----- 286

QY 301 RAMISRWFYDVTGKCAFFYGGCGGNRNFDTBEYCMAYCGSVMSLLKTTQFHLPOD 360
DB 301 RAMISRWFYDVTGKCAFFYGGCGGNRNFDTBEYCMAYCGSVMSLLKTTQFHLPOD 360

QY 289 ---VPTTAATPDPAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 345
DB 289 ---VPTTAATPDPAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 345

QY 361 PVKLPTTAATPDPAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 420
DB 361 PVKLPTTAATPDPAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 420

QY 346 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHARVEAMLDNRRLALENYITAL 405
DB 346 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHARVEAMLDNRRLALENYITAL 405

QY 421 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHARVEAMLDNRRLALENYITAL 460
DB 421 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHARVEAMLDNRRLALENYITAL 460

QY 406 QAVPPRPRHVFNMUKYVRAEQDKRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRIYER 465
DB 406 QAVPPRPRHVFNMUKYVRAEQDKRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRIYER 465

QY 481 QAVPPRPRHVFNMUKYVRAEQDKRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRIYER 540
DB 481 QAVPPRPRHVFNMUKYVRAEQDKRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRIYER 540

QY 466 MNQSLSLYNPVAAEEIQDEVDELLOKEQNSDDVLNMISEPRISYGNDAIMPSTLET 525
DB 466 MNQSLSLYNPVAAEEIQDEVDELLOKEQNSDDVLNMISEPRISYGNDAIMPSTLET 525

QY 541 MNQSLSLYNPVAAEEIQDEVDELLOKEQNSDDVLNMISEPRISYGNDAIMPSTLET 600
DB 541 MNQSLSLYNPVAAEEIQDEVDELLOKEQNSDDVLNMISEPRISYGNDAIMPSTLET 600

QY 526 KTIIVELLPVNGEFSLDDIOPWHPPFCVDSVPANTENFEPVDARPAADRGLTIRPGSLTN 585

DB 601 KTIIVELLPVNGEFSLDDIOPWHPPFCVDSVPANTENFEPVDARPAADRGLTIRPGSLTN 660
QY 586 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLVKGWVIATVIFIL 645
DB 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLVKGWVIATVIVIL 720
QY 646 VMLKKKQVTSIHGGVVVVDAAVTPERHLKMQQNGYENPTYKFEQMN 595
DB 721 VMLKKKQVTSIHGGVVVVDAAVTPERHLKMQQNGYENPTYKFEQMN 770

RESULT 4
Q9DQ38 PRELIMINARY: PRT; 695 AA.
AC Q9DQ38;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodollos A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1;
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 93.7%; Score 3423; DB 13; Length 695;
Best Local Similarity 93.8%; Pred. No. 3.7e+199;
Matches 654; Conservative 17; Mismatches 22; Indels 4; Gaps 3;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONWCKGRKCKOCTHHPFVYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONWCKGRKCKOCTHHPFVYRCVLG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNLJPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNLJPCGIDKFR 180

QY 181 GFVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEAEVEE 238
DB 181 GFVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEAEVEE 240

QY 239 ESEACDDEDEDGDEVEEAEPYEATERTTSIATTTTTTIESVEEYVVRPTTAATPD 298
DB 241 DEADDD--DODDGDDEI--EETEEYEATERTTSIATTTTTTIESVEEYVVRPTTAATPD 298

QY 299 AYDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAQNLKADKAVIQ 358
DB 299 AYDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAQNLKADKAVIQ 358

QY 359 HFQEKVESLEQEAANERQQLVETHARVEAMLDNRRLALENYITALQAVPPRPRHVFNM 418
DB 359 HFQEKVESLEQEAANERQQLVETHARVEAMLDNRRLALENYITALQAVPPRPRHVFNM 418

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Db 359 HFQKVESLEGEAANERQOLVETHMARVEAMINDERRIALENYITALQTVPPRRIVFNM 418
QY 419 LKYYVRAQKDRQHTLKHFEHRVMYDPKKAQIRISQVMTHLRVYIERMNS:SLLYNVA 478
Db 419 LKYYVRAQKDRQHTLKHFEHRVMYDPKKAQIRISQVMTHLRVYIERMNS:SLLYNVA 478
QY 479 VAEETODEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGE 538
Db 479 VAEETODEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGE 538
QY 539 SDDQLQPHSGADSVAPANTENEPEVDARPAADRGLTTRPGSLTNIKTEISEVKMDA 598
Db 539 SDDQLQPHSGADSVAPANTENEPEVDARPAADRGLTTRPGSLTNIKTEISEVKMDA 598
QY 599 EFRHDSGYEVHRQKLVFFAEVDSGSKGAILGLMVGGVVIAIV:PIITLVMLKKQYTSIHH 658
Db 599 EFRHDSGYEVHRQKLVFFAEVDSGSKGAILGLMVGGVVIAIV:PIITLVMLKKQYTSIHH 658
QY 659 GYVEVDAVTPERHLSKMQONGYENPTYKFEQMON 695
Db 659 GYVEVDAVTPERHLSKMQONGYENPTYKFEQMON 695

RESULT 5
Q9DGT7
ID Q9DGT7 PRELIMINARY; PRI: 751 AA.
AC Q9DGT7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodoloso A., Serribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/CCBJ databases.
DR EMBL; AF289219; AAG00594.1;
DR HSSP; P05067; LB44
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BP1.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPT1; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR Prodom; PD000222; Kunitz_BP1; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; K3; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE; PS00279; BPT1_KUNITZ_2; 1.
KW protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 92.6%; Score 3382; DB 13; Length 751;
Best Local Similarity 86.7%; Pred. No. 1.2e-196;
Matches 653; Conservative 18; Mismatches 22; Indels 60; Gaps 4;

QY 1 MFLPGALLLAAWTARALEVPTDGNAGLLAEPOIAFMFCGRINMHNMYONGKWDSDPGTK 60
Db 1 MFLPGALLLAAGAAAEVPAADGNAGLLAEPOIAFMFCGRINMHNMYONGKWDSDPGTK 60
QY 61 TCIDTKEGILQYCOEYPELQITNVVEANQPTVIONCKKCKCKTQHPHFVIPYKCLV 120
Db 61 TCIDTKEGILQYCOEYPELQITNVVEANQPTVIONCKKCKCKTQHPHFVIPYKCLV 120

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QY 121 EFVSDALLVPCKFLQIQRMDVCETHLHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPCKFLQIQRMDVCETHLHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFFVCCPLAESDNYSDADEDDSDVMWGADTDYADGSDKVVVE--VAEEEEEVAEVE 238
Db 181 GVEFFVCCPLAESDNYSDADEDDSDVMWGADTDYADGSDKVVVE--VAEEEEEVAEVE 238
QY 239 EEEADDDDEDDGDEVEEAEPEYEATEKTSTTSIATTTTTSVSEVEWR----- 288
Db 241 DEDADDD--DDDDGDEI-BETEEYEATEKTSTTSIATTTTTSVSEVEWR----- 288
QY 289 -----VPTTAASTPRADVK 302
Db 299 PCRAMISRWYFDVAGKCAPFFYGGCGGNRNFDSSEYCMVAGSVLPTTAASTPRADVK 358
QY 303 YLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHFE 362
Db 359 YLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHFE 418
QY 363 KVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKKY 422
Db 419 KVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKKY 478
QY 423 VRAEQKDRQHTLKHFEHRVMYDPKKAQIRSOVMTHLRVYIERMNS:SLLYNVAEAE 482
Db 479 VRAEQKDRQHTLKHFEHRVMYDPKKAQIRSOVMTHLRVYIERMNS:SLLYNVAEAE 538
QY 483 QDEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGEFLDD 542
Db 539 IQDEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGEFLDD 598
QY 543 LQPHSFGAOSVPANTENEPEVDARPAADRGLTTRPGSLTNIKTEI1SEVKMDAEFRH 602
Db 599 LQPHSFGAOSVPANTENEPEVDARPAADRGLTTRPGSLTNIKTEI1SEVKMDAEFRH 658
QY 603 DSGYEVHRQKLVFFAEVDSGSKGAILGLMVGGVVIAIV:PIITLVMLKKQYTSIHHQWE 662
Db 659 DSGYEVHRQKLVFFAEVDSGSKGAILGLMVGGVVIAIV:PIITLVMLKKQYTSIHHQWE 718
QY 663 VDAAVTPERHLSKMQONGYENPTYKFEQMON 695
Db 719 VDAAVTPERHLSKMQONGYENPTYKFEQMON 751

RESULT 6
Q98SGO
ID Q98SGO PRELIMINARY; PRI: 693 AA.
AC Q98SGO;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein A.
GN APP.
CS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1;
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.

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DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C:AB653 CRC64;

Query Match      87.8%; Score 3209; DB 13; Length 695;
Best Local Similarity 87.7%; Pred. No. 3.4e-186;
Matches 61; Conservative 36; Mismatches 44; Indels 5; Gaps 4;

QY 1 MLPGLALLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLNMMHVQNGKWDSPSGTK 60
DB 1 MLPHTLLVLTV-GALA-EVPADCGLLAEPOIAMFCGKLNMMHVQNGKWEIDVSGTK 59

QY 61 TCIDTKGILQYCOEYVPELOITNVVEANQPVTTIONMCKGRKCKOCTHPIHFVPIYRCLVG 120
DB 60 GCIGTKGILQYCOEYVPELOITNVVEANQPVTTIONMCKGRKCKOCTHPIHFVPIYRCLVG 119

QY 121 EFVSDALLVPDKCFHQRERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
DB 120 EFVSDALLVPDKCFHQRERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 179

QY 181 GVEFVCCPAAEESDNVDSADAEDSDVWVGADIDYADGSEDKVVEA--EEFEVAAVE 238
DB 180 GVEFVCCPAAEESSEFSADA-EDSDVWVGADYVDRSDCKAVEAQPUSEEEVVE 238

QY 239 EEEADDDDDGDEVEEAEPEEATERTTSTATTTTTTSTESVEEVVVPVTAASIPD 298
DB 239 EEEADDDDD--DGFDAEEPEEPEEATERTTSTATTTTTTSTESVEEVVVPVTAASIPD 296

QY 299 AVDKYLETPGDENEHAFQKAKERLEAKHREMSQVMEAEERQAKNLPKADKKAVIQ 358
DB 297 AVDKYLENFNDENEHDFLKAKERLEGKHKREKMEVMEAEERQAKNLPKADKKAVIQ 356

QY 359 HFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENM 418
DB 357 HFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQADPPRPRHVENM 416

QY 419 LKKYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNVPA 476
DB 417 LKKYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNVPA 476

QY 479 VAEETQDEVDLLOKEQNSDDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEF 532
DB 477 VAEETQDEVDLFOKEQNSDDVSNVMSVDRHSYGNDAIMPSTETKTVELLPVNGEF 535

QY 539 SLDDI:QPHWISFGADSVANTENEVEPVDARPAADRGITTRPGSGITNKTETISEVKMDA 598
DB 537 NIEDLQPHWISFGVDSVPANTENEVEPVDARPAADRGITTRPGSGITNKTETISEVKMD 596

QY 599 EFRHDSGVEVHHQKLVFFAEVGSNGKGAIGLMVGGVVIATVITLVMKKKCYTIIH 659
DB 597 EYRHTAYEVHHQKLVFFAEVGSNGKGAIGLMVGGVVIATVITLVMKKKCYTIIH 656

QY 659 GVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 695
DB 657 GWEVDAAVTPEERHLTKMQONGYENPTYKFFEQMQN 693

RESULT 7
Q98SF9
AC Q98SF9; PRELIMINARY; PRT; 695 AA.
DT 01-JUN-2001 (TReMBLrel. 17. Created)
DT 01-JUN-2001 (TReMBLrel. 17. Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22. Last annotation update)
DE Beta-amyloid precursor pro-ein B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

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RESULT 8

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051963
ID Q91963 PRELIMINARY: PRT: 747 AA.
AC Q91963
DT 01-NOV-1995 (TrEMBLrel. 0., Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xeropodinae.
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A. PubMed:1282805;
RX MEDLINE-93129227; PubMed:1282805;
RA Okada H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL: S52417; AAB24853.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_RPT1.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_RPT1; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRODOM: PS000222; Kunitz_RPT1; 1.
DR SMART: SM00131; Kunitz; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor;
SQ SEQUENCE 747 AA; 84893 MW; A75E8185681D948 CRC64;

Query Match 84.6%; Score 3098; DB 13; Length 747;
Best Local Similarity 80.7%; Pred. No. 1.9e-179;
Matches 597; Conservative 35; Mismatches 42; Indels 64; Gaps 5;

QY 17 ALEVPTDGNAGLLAEPOIANF-CGRLNHNNVQNGKNDSPSGTKTKIDTKEGILQYQCE 75
DB 15 ALEVLGNGLLAEPOIANFVSVARLNHNNVQNGKWTQVSG--CIGTKEGILQYQCE 71
QY 76 VYPELQITNVVEANQPTVIONWCKGRKQCKTDPHFVPIYRCLVGEVSDALVPOCKKF 135
DB 72 VYPELQITNVVEANQPTVIONWCKGRKQCKSRTHIVPYRCLVGEVSDALVPOCKKF 13;
QY 136 LHOQEMDVCEHLHWHHTVAKETSEKSTNLHDYGMLLPCGIDKFRGVFFVCCPLAESDN 195
DB 132 LHOQEMDICETHLHWHHTVAKESKESKMSLHEYGMLTFCGIDKFRGVFFVCCPSABES 191
QY 196 VDSADAECDSDVWVGADTDYADGSDCKVVEVA--EEERVAEVEEAEADDDDEGQF 253
DB 192 FDSADAECDSDVWVGADTDYADGSDCKVVEVA--EEERVAEVEEAEADDDDEGQF 249
QY 254 VEERAEPEYEDATERITSIATITTTTTTSEVVEVVR-----VPTTAASTPDVVDKYLETSGDENEHAFQ 317
DB 250 AEERPEPEYEDATERITSIATITTTTTTSEVVEVVR-----VPTTAASTPDVVDKYLETSGDENEHAFQ 309
QY 289 -----VPTTAASTPDVVDKYLETSGDENEHAFQ 317
DB 310 SKCAQFIYGGCGGNRNFFESDVCYAVGSGVIPATAASTPDVVDKYLENPDNENEHDFL 369
QY 318 KAKERLEAKHRERMSQVMEERAEERAKNLPRADKKAIVQHFQEKVESLEQEAAENERQ 377
DB 370 KAKERLECKHEKKESEVYKENEERAEERAKNLPRADKKAIVQHFQEKVESLEQEAAQORQ 429
QY 378 LVETIHARVEAMLNDRRLALENIYITALQAVPRPRHFNMLKKYVRAEQDKRQHTLKHF 437
DB 378 LVETIHARVEAMLNDRRLALENIYITALQAVPRPRHFNMLKKYVRAEQDKRQHTLKHF 437

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DB 430 LVETIHARVEAMLNDRRLALENIYITALQAVPRPRHFNMLKKYVRAEQDKRQHTLKHF 439
QY 438 EHRMVDPKKAQIRSQVNTHLRVLYERNOSLSLLYNYPVAVAEIQDEVDLLOKEQNY 497
DB 490 EHRMVDPKKAQIRSQVNTHLRVLYERNOSLSLLYNYPVAVAEIQDEVDLLOKEQNY 549
QY 498 SDDVLANNISEPRISYGNDALMPSLTETKTVELLPVNGEFSLDLQOPWHSFGADSVAN 557
DB 550 SDDVMNVSVDHRVSGNDALMPSLTETKTVELLPVNGEFSLDLQOPWHSFGADSVAN 609
QY 558 TENEVPEVDARPAADRGLTIRPGSLTNIKTEEISEVKMDAEFRHDSGYEVIHOKLVFFA 617
DB 610 TENEVPEVDARPAADRGLTIRPGSLTNIKTEEISEVKMDSEYRHDATAYEVHOKLVFFA 669
QY 618 EDVGSNKGAIGLVMGVVVIATVITVLMLKKKYTSIHHGVVEVDAAVTPEERHLSKM 677
DB 670 EEVGSNKGAIGLVMGVVVIATVITVLMLKKKYTTIHHGVVEVDAAVTPEERHLTKM 729
QY 678 QONGYENPTYKFFEQMON 695
DB 730 QONGYENPTYKFFEQMON 747

RESULT 9
Q57394 PRELIMINARY: PRT: 699 AA.
AC Q57394;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE EL amyloid precursor protein 699.
GN EL APP699.
OS Närke Japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualia; Pristiogaster; Batoidae;
OC Torpediniformes; Narcinoidae; Narkidae; Närke.
OX NCBI_TaxID=62965;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Electric lobe;
RX MEDLINE-98129705; PubMed=9461486;
RA Tijiwa K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA Suzuki T.;
RT "CDNA isolation of Alzheimer's amyloid precursor protein from
RT cholinergic nerve terminals of the electric organ of the electric
RT ray.";
KL Biochem. J. 330:29-33(1998).
DR EMBL: AB005544; BAA24230.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;

Query Match 81.0%; Score 2959.5; DB 13; Length 699;
Best Local Similarity 80.7%; Pred. No. 4.4e-171;
Matches 568; Conservative 58; Mismatches 59; Indels 19; Gaps 8;

QY 2 LRG-LALLLLAANTA-----RALEVPTDGNAGLL-NEPOIANFPCGRLNHNNVQNGK 52
DB 5 LRGRLGMLLLAALAAALVLAFLAPLRALEVPTDGNAGLLAALAEPOIANFPCGRLNHNNVQNGK 64
QY 53 DSDPSGKTCTIDTKEGILQYQCEVPELQITNVVEANQPTVIONWCKGRKQCKTDPHFV 112
DB 65 VSDPSGKTCTIDTKEGILQYQCEVPELQITNVVEANQPTVIONWCKGRKQCKTDPHFV 124
QY 113 IPYRCLVGEVSDALVPOCKKFLHQRMDVCETHLHWHHTVAKETSEKSTNLHDYGMLL 172
DB 113 IPYRCLVGEVSDALVPOCKKFLHQRMDVCETHLHWHHTVAKETSEKSTNLHDYGMLL 172
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125 VPKCLVGEFVSALVYPCKFLHREKMDTCESHLWETIVAKETGDKIMNLDYGMLL 184
173 PCGIDKRGVEFVCCPLAESDMMVDSADAEDSDVMWGGADTDYADGSDKVEVAEE 232
185 PCGIDFGRGVEFVCCPIPEENDKIDS-DMDESDVMWGGDDADYAGG-DKTV---EE 236
233 EVAEEEDDDDEDDGDEVEE-EEEPYEATERITISATITTTTSSVEEVVRPT 291
239 KPIEEEDDESIDDEWUCLDDDEVVDQYEPTEETIS--SITTTTSA:BEVVRPT 295
292 TAASIPDAVKYLETGCDENEHAFQAKERLEAKHERMSQVMREAEFROAKNLPKA 351
296 TAASIPDAVKYLETGCDENEHAFQAKERLEAKHERMSKIMREWEAEFROAKNLPKA 355
352 DKKAVIQHFOEKVESLQEAANERQQLVETIMARVEAMLNDRRRLALENYITALQAVPPK 411
356 DKKAVIOFQOMVESLQEAANERQQLVETIMARVEAMLNDRRRLALENYITALQADPPK 415
412 PRHVENMLKYYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLS 471
416 PRHVLNALKKYSRAEQDRQHTLKHFEHVRMVDPEKAAQIKSOVMTHLRVIERMNSQSLS 475
472 LLNVPAVAEIDQVDELLOKEQNSDDVLANNMISPRISYNDALMPSLTETKTIVEL 531
476 LLKVPVSAEIQDEVDLLOKEQNSDDVLANNMISPRISYNDALMPSLTETKTIVEL 535
532 LPVNGESLDDLOPHWSFGADSPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI 591
536 LPDGGELFLLDLOPHWFVIESIPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI 595
592 SEVKMDAEFRHDSQYEVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITVLMKKK 651
596 AEKMETEFQDQSGYEVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVITVLMKKK 655
652 QYTSIHGGVVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMN 695
656 QYTSIHGGVVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMN 699

RESULT 10
Q9PVL1 PRELIMINARY: PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RI "What the evolution of the amyloid protein precursor: supergene family
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; PG5067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PS00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match: 75.6%; Score 2762.5; DB 13; Length 569;

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Best Local Similarity 93.4%; Pred. No. 2.8e-159;
Matches 534; Conservative 14; Mismatches 19; Indels 5; Gaps 4;

QY 126 ALLVPDKCKFLHREKMDVCETHLHHTVAKETCSEKSTNLDHYGMLLPCGIDKRGVEFV 185
DB 1 ALLVPDKCKLLHREKMDVCETHLHHTVAKESSEKSNLDHYGMLLSCGIDKRGVEFV 60
QY 186 CCPLAESDMMVDSADAEDSDVMWGGADTDYADGSDKVE--VAEEVEAEVEEEDAD 243
DB 61 CCPLAESDNLDSADAEDSDVMWGGADADYADGSDKVEEQPEDEELTWEDDEDAD 120
QY 244 DDEDDGDEVEEAEPEEATEITSTATITTTTSSVEEVVRPTAASIPDAVKY 303
DB 121 DD-DDDDGDEI-EETEEYEAEATEITSTATITTTTSSVEEVVRPTAASIPDAVKY 178
QY 304 LETPGDENEHAFQAKERLEAKHERMSQVMREWEAEFROAKNLPKADKAVIQHFOEK 363
DB 179 LETPGDENEHAFQAKERLEAKHERMSQVMREWEAEERQAKNLPKADKAVIQHFOEK 236
QY 364 VESLQEAANERQQLVETIMARVEAMLNDRRRLALENY:TALQAVPPRPRHVRMNLKYYV 423
DB 239 VESLQEAANERQQLVETIMARVEAMLNDRRRLALENY:TALQAVPPRPRHVRMNLKYYV 298
QY 424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYVPAVAEEI 463
DB 299 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSFYVPAVAEEI 358
QY 484 QDEVDLLOKEQNSDDVLANNMISPRISYNDALMPSLTETKTIVELLPVNGESLDDL 543
DB 359 QDEVDLLOKEQNSDDVLANNMISPRISYNDALMPSLTETKTIVELLPVNGESLDDL 418
QY 544 QPHWSFGADSPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 603
DB 419 QPHWSFGADSPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 478
QY 604 SGYEVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITVLMKKKKOYTSIHGGVVEV 663
DB 479 SGYEVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVITVLMKKKKOYTSIHGGVVEV 538
QY 664 DAAVTPPEERHLSKMQONGYENPTYKFFEQMN 695
DB 539 DAAVTP-ERHLSKMQONGYENPTYKFFEQMN 569

RESULT 11
Q99K32 PRELIMINARY: PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 68.4 kDa protein (fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
KL Submitted (MAR-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC005490; AAH05490.1; -.
DR HSSP; P05067; 2AAP.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.

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DR SMART: SMO0131: KU: 1
DR PROSITE: PS00319; A4_EXTRA: 1.
DR PROSITE: PS00320; A4_INTRA: 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1: 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2: 1.
DR Hypothetical protein; protease inhibitor; Serine protease inhibitor.
DR NON_TER 1
FT
SQ SEQUENCE 607 AA: 68391 MW: 86391 MW: BF802214CSA7D172 CRC64;

Query Match 72.0%; Score 2630.5; DB 11; Length 607;
Best Local Similarity 85.5%; Pred. No. 3e-151;
Matches 519; Conservative 4; Mismatches 9; Indels 75; Gaps 1;

QY 164 NLHDYGMLLPGGIDKFGVGVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSD 223
DB 1 NLHDYGMLLPGGIDKFGVGVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSD 60
QY 224 KVEVEAEVEAEVEAEADDEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 283
DB 61 KVEVEAEVEAEVEAEADDEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 120
QY 284 EENVV----- 288
DB 121 EENVVVCSEQATGCPGRAMISRWYFDVTEGKCVPEFYGGCGGNRNFTVYCMVCGS 180
QY 289 -----VPTTAASTPDVAVDKY-ETPGDENEHAHFQKAKERLEAKHR 328
DB 181 VSTOSLLKTTSELPQDFDKLPTTAASTPDVAVDKYLETGPDENEHAHFQKAKERLEAKHR 240
QY 329 ERMQVWREWEAEERQAKNLPKADKKAVIOHFQKVESLEGEAANERQQLVEHMARVEA 386
DB 241 ERMQVWREWEAEERQAKNLPKADKKAVIOHFQKVESLEGEAANERQQLVEHMARVEA 300
QY 389 MLNDRRLALENYITALCAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKA 446
DB 301 MLNDRRLALENYITALCAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKA 360
QY 449 AQHSQVWTHLRVYIERKNSLSLLYNVPAVAEIODEVDELQKQNSDDVLANKNISE 506
DB 361 AQHSQVWTHLRVYIERKNSLSLLYNVPAVAEIODEVDELQKQNSDDVLANKNISE 420
QY 509 PRISYGNDAIMPSTETKITVELLPVNGEFLSDLOQPHWSEFGADSVDPANTENEVEPVDAR 569
DB 421 PRISYGNDAIMPSTETKITVELLPVNGEFLSDLOQPHWSEFGADSVDPANTENEVEPVDAR 480
QY 569 PAADRGTLTRPGSLTNKTEIIESEVKMDAEFRHDSQYEVHGHKLVFFAEVGSNKGAT 628
DB 481 PAADRGTLTRPGSLTNKTEIIESEVKMDAEFRHDSQYEVHGHKLVFFAEVGSNKGAT 540
QY 629 GLMVGGVVIATVIFITILVMLKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYK 588
DB 541 GLMVGGVVIATVIFITILVMLKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYK 600
QY 689 FFFQMQN 695
DB 601 FFEQMQN 607

RESULT 12
O93296 PRELIMINARY; PRT; 534 AA.
AC O93296
DI 01-NOV-1998 (TREMBLrel. 08, Created)
DI 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
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PX MEDLINE-98337885; PubMed-9671674;
RA Barnes N.Y.; Li L.; Yoshikawa K.; Schwartz L.M.; Oppenheim R.W.;
RA Milligan C.E.;
RI "Increased production of amyloid precursor protein provides a
K: substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1;
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR NON_TER 1
FT
SQ SEQUENCE 534 AA: 60597 MW: FB53ECC2E66D4C92 CRC64;

Query Match 71.4%; Score 2608; DB 13; Length 534;
Best Local Similarity 94.6%; Pred. No. 5.9e-150;
Matches 505; Conservative 13; Mismatches 12; Indels 3;

QY 164 NLHDYGMLLPGGIDKFGVGVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSD 223
DB 3 NLHDYGMLLPGGIDKFGVGVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSD 62
QY 224 KVEVEAEVEAEVEAEADDEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 281
DB 63 KVEVEAEVEAEVEAEADDEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 120
QY 282 SYEEVVRVPTTAASTPDVAVDKYLETGPDENEHAHFQKAKERLEAKHRMSQVWREWEA 341
DB 121 SYEEVVRVPTTAASTPDVAVDKYLETGPDENEHAHFQKAKERLEAKHRMSQVWREWEA 180
QY 342 ERQAKNLPKADKKAVIOHFQKVESLEGEAANERQQLVEHMARVEAMLNDRRLALENY 401
DB 181 ERQAKNLPKADKKAVIOHFQKVESLEGEAANERQQLVEHMARVEAMLNDRRLALENY 240
QY 402 ITALQAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKAQIRSQVWTHLRV 461
DB 241 ITALQAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKAQIRSQVWTHLRV 300
QY 462 IYERNQSLSLYLVNVPVAEIODEVDELQKQNSDDVLANKNISEPRISYGNDAIMP 521
DB 301 IYERNQSLSLYLVNVPVAEIODEVDELQKQNSDDVLANKNISEPRISYGNDAIMP 360
QY 522 JTETKITVELLPVNGEFLSDLOQPHWSEFGADSVDPANTENEVEPVDARPAADRGTLTRPG 581
DB 361 JTETKITVELLPVNGEFLSDLOQPHWSEFGADSVDPANTENEVEPVDARPAADRGTLTRPG 420
QY 582 GLTNKTEIIESEVKMDAEFRHDSQYEVHGHKLVFFAEVGSNKGATIGLVGGVVIATVI 641
DB 421 GLTNKTEIIESEVKMDAEFRHDSQYEVHGHKLVFFAEVGSNKGATIGLVGGVVIATVI 480
QY 642 FILLVMLKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYKFFEQMQN 695
DB 481 FILLVMLKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYKFFEQMQN 534

RESULT 13
O73683 PRELIMINARY; PRT; 780 AA.
AC O73683
DI 01-AUG-1998 (TREMBLrel. 07, Created)
DI 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; percomorpha; Tetraodontiformes;
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OC Tetradontoidae; Tetradontidae; Tetradontom.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252138; PubMed=9599080;
RT Villard L., Tassone P., Cnognorac-Jurcevic T., Clancy K., Gardiner K.;
RA Analysis of pufferfish homologues of the AT-rich human APP gene.;
RL Gene 210:17-24(1998).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
CC BPTI/KUNITZ FAMILY OF INHIBITORS.
CC DR EMBL: AFO18165; AAC41275.1; -.
DR HSSP: P05067; 1H23.
DR DR INTERPRO: IPR001868; A4_APP.
DR DR INTERPRO: IPR001255; Beta-APP.
DR DR INTERPRO: IPR002223; Kunitz_BPTI.
DR DR Pfam: PF03494; Beta-APP; 1.
DR DR Pfam: PF00014; Kunitz_BPTI; 1.
DR DR PRINTS: PR00203; AMYLOIDA4.
DR DR PRINTS: PR00759; BASICPTASE.
DR DR PRODOM: PD000222; Kunitz_BPTI; 1.
DR DR SMART: SM00006; A4_EXTRA; 1.
DR DR SMART: SM00131; KU; 1.
DR DR PROSITE: PS00319; A4_EXTRA; 1.
DR DR PROSITE: PS00320; A4_INTRA; 1.
DR DR PROSITE: PS00280; BPTI_KUNITZ_1; FALSE_NFG.
DR DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Serine protease inhibitor.
FT SIGNAL 1 18
FT CHAIN 19 780
FT FT
FT CHAIN 682 724
FT DOMAIN 719 711
FT TRANSMEM 712 732
FT DOMAIN 733 780
FT DOMAIN 733 382
FT SITE 769 772
FT DISULFID 327 378
FT DISULFID 336 361
FT CARBOHYD 563 560
FT SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;
SO QUERY MATCH
Best Local Similarity 70.3%; Score 2568; DB 13; Length 780;
Matches 512; Conservative 71; Mismatches 95; Indels 106; Gaps 10;
QY 7 LLLLAANTALEVPIIDGNAGLLAPQIAMFCGRUMEMVQNGKWDSPSGTKTCIDTK 66
DB 8 LLLVAASNTLAAEVPITDVSMLLAEPQVAFGCKINHHINVOGKWEPEPSCSKCIGTK 67
QY 67 EGILCYCEVYPELOITNVVEANQVPTIONCKCRKCKTHPHVPIYRCINGEFVSDA 126
DB 68 EGILQICQVYPELOITNVVEANQVPTIONCKCRKCKTHPHVPIYRCINGEFVSDA 127
QY 127 LLVPDKCKFLHQRMDVCFTHLRKHTVAKETCSKSTNLHDYGMLLPGCIDPKFRGVFVC 186
DB 128 LLVPDKCKFLHQRMNQCESHLHHTVAKESCGDRAMNLDYGMLLPGCIDPKFRGVFVC 187
QY 187 CPLAESDNVDGADAEEDSDVWNGAGDITVDGDS-----EKKVVEVAEE 232
DB 188 CP-AEAERMDSTEDADSDSDVWNGADNDYSDNSWVRZPEFAEQOEETRPVSVVEEEEG 246

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QY 653 YTSIHGVEYDAAVTPERHLSKMQONGYENPTYKFFEQMON 695
DE 652 YTS-HHGVEYDAAVTPERHLAKMQONGYENPTYKFFEQMON 694

Search completed: October 2, 2003, 14:02:40
Job time : 41 secs